

TITLE

Novel Genes Encoding Proteins Having Prognostic, Diagnostic,
Preventive, Therapeutic, And Other Uses

5 CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application serial number 09/578,063, filed on May 24, 2000, which is a continuation-in-part of U.S. Application serial number 09/333,159, filed on June 14, 1999.

10 This application is also a continuation-in-part of U.S. Application serial number 09/596,194, filed on June 16, 2000, which is a continuation-in-part of U.S. Application serial number 09/342,364, filed on June 29, 1999.

This application is also a continuation-in-part of U.S. Application serial number 09/608,452, filed on June 30, 2000, which is a continuation-in-part of U.S. Application serial number 09/393,996, filed on September 10, 1999.

15 This application is also a continuation-in-part of U.S. Application serial number 09/345,680, filed on June 30, 1999.

The contents of each of the applications cross-referenced in this section are incorporated into this disclosure by reference.

20 STATEMENT REGARDING FEDERAL RESEARCH SUPPORT

Not Applicable

REFERENCE TO MICROFICHE APPENDIX

Not Applicable

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BACKGROUND OF THE INVENTION

The molecular bases underlying many human and animal physiological states (e.g., diseased and homeostatic states of various tissues) remain unknown.

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Nonetheless, it is well understood that these states result from interactions among the proteins and nucleic acids present in the cells of the relevant tissues. In the past, the complexity of biological systems overwhelmed the ability of practitioners to understand the molecular interactions giving rise to normal and abnormal physiological states. More recently, though, the techniques of molecular biology, transgenic and null mutant animal production, computational biology, and pharmacogenomics have enabled practitioners to discern the role and importance of individual genes and proteins in particular physiological states.

Knowledge of the sequences and other properties of genes (particularly including the portions of genes encoding proteins) and the proteins encoded thereby enables the practitioner to design and screen agents which will affect, prospectively or retrospectively, the physiological state of an animal tissue in a favorable way. Such knowledge also enables the practitioner, by detecting the levels of gene expression and protein production, to diagnose the current physiological state of a tissue or animal and to predict such physiological states in the future. This knowledge furthermore enables the practitioner to identify and design molecules which bind with the polynucleotides and proteins, in vitro, in vivo, or both.

Many secreted proteins, for example, cytokines and cytokine receptors, play a vital role in the regulation of cell growth, cell differentiation, and a variety of specific cellular responses. A number of medically useful proteins, including erythropoietin, granulocyte-macrophage colony stimulating factor, human growth hormone, and various interleukins, are secreted proteins. Thus, an important goal in the design and development of new therapies is the identification and characterization of secreted and transmembrane proteins and the genes which encode them.

Many secreted proteins are receptors which bind a ligand and transduce an intracellular signal, leading to a variety of cellular responses. The identification and characterization of such a receptor enables one to identify both the ligands which bind to the receptor and the intracellular molecules and signal transduction pathways

associated with the receptor, permitting one to identify or design modulators of receptor activity, e.g., receptor agonists or antagonists and modulators of signal transduction.

SUMMARY OF THE INVENTION

The present invention is based, at least in part, on the discovery of human cDNA molecules which encode proteins which are herein designated TANGO 273, TANGO 325, TANGO 364, TANGO 405, and M019 (M019 is synonymous with TANGO 533). These proteins, fragments thereof, derivatives thereof, and variants thereof are collectively referred to herein as the polypeptides of the invention or the proteins of the invention. Nucleic acid molecules encoding polypeptides of the invention are collectively referred to as nucleic acids of the invention.

The nucleic acids and polypeptides of the present invention are useful as modulating agents for regulating a variety of cellular processes. Accordingly, in one aspect, the present invention provides isolated nucleic acid molecules encoding a polypeptide of the invention or a biologically active portion thereof. The present invention also provides nucleic acid molecules which are suitable as primers or hybridization probes for the detection of nucleic acids encoding a polypeptide of the invention.

The invention also includes fragments of any of the nucleic acids described herein wherein the fragment retains a biological or structural function by which the full-length nucleic acid is characterized (e.g., an activity, an encoded protein, or a binding capacity). The invention furthermore includes fragments of any of the nucleic acids described herein wherein the fragment has a nucleotide sequence sufficiently (e.g., 50%, 60%, 70%, 80%, 85%, 90%, 95%, 98%, or 99% or greater) identical to the nucleotide sequence of the corresponding full-length nucleic acid that it retains a biological or structural function by which the full-length nucleic acid is characterized (e.g., an activity, an encoded protein, or a binding capacity).

5 The invention also includes fragments of any of the polypeptides described herein wherein the fragment retains a biological or structural function by which the full-length polypeptide is characterized (e.g., an activity or a binding capacity). The invention furthermore includes fragments of any of the polypeptides described herein wherein the fragment has an amino acid sequence sufficiently (e.g., 50%, 60%, 70%, 80%, 85%, 90%, 95%, 98%, or 99% or greater) identical to the amino acid sequence of the corresponding full-length polypeptide that it retains a biological or structural function by which the full-length polypeptide is characterized (e.g., an activity or a binding capacity).

10 The invention also features nucleic acid molecules which are at least 40% (or 50%, 60%, 70%, 80%, 90%, 95%, or 98%) identical to the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, and 82, the human TANGO 273 nucleotide sequence of the cDNA insert of a clone deposited on April 2, 1999 with the American Type Culture Collection® (ATCC®) as accession no. 207185, the murine TANGO 273 nucleotide sequence of the cDNA insert of a clone deposited on April 2, 1999 with ATCC® as accession no. 207221, the human TANGO 325 nucleotide sequence of the cDNA insert of a clone deposited on May 28, 1999 with ATCC® as accession no. PTA-147, the human TANGO 364 nucleotide sequence of the cDNA insert of a clone deposited on July 23, 1999 with ATCC® as accession no. PTA-425, the human TANGO 405 nucleotide sequence of the cDNA insert of a clone deposited on July 23, 1999 with ATCC® as accession no. PTA-424, the murine TANGO 405 nucleotide sequence of the cDNA insert of a clone deposited on ____ with ATCC® as accession no. ____, the human M019 nucleotide sequence of the cDNA insert of a clone deposited on ____ with ATCC® as accession no. ____, or a complement thereof. These deposited nucleotide sequences are hereafter individually and collectively referred to as "the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ____, and ____."

The invention features nucleic acid molecules which include a fragment of at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more) consecutive nucleotide residues of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof.

The invention also features nucleic acid molecules which include a nucleotide sequence encoding a protein having an amino acid sequence that is at least 50% (or 60%, 70%, 80%, 90%, 95%, or 98%) identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof.

In certain embodiments, the nucleic acid molecules have the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___.

Also within the invention are nucleic acid molecules which encode a fragment of a polypeptide having the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, the fragment including at least 10 (12, 15, 20, 25, 30, 40, 50, 75, 100, 125, 150, 200, 250, 300, 400, 500, 750, 1000 or more) consecutive amino acid residues of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85.

The invention includes nucleic acid molecules which encode a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, wherein

the nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule having a nucleic acid sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, 5 PTA-425, PTA-424, ___, and ___, or a complement thereof.

Also within the invention are isolated polypeptides or proteins having an amino acid sequence that is at least about 50%, preferably 60%, 75%, 90%, 95%, or 98% identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85.

10 Also within the invention are isolated polypeptides or proteins which are encoded by a nucleic acid molecule having a nucleotide sequence that is at least about 40%, preferably 50%, 60%, 75%, 85%, or 95% identical to the nucleic acid sequence encoding any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, and isolated polypeptides or proteins which are encoded by a nucleic acid molecule consisting of the nucleotide sequence which hybridizes under stringent 15 hybridization conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___.

20 Also within the invention are polypeptides which are naturally occurring allelic variants of a polypeptide that includes the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ 25 ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof.

The invention also features nucleic acid molecules that hybridize under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof. In other embodiments, the nucleic acid molecules are at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more) nucleotides in length and hybridize under stringent conditions to a nucleic acid molecule having the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof. In some embodiments, the isolated nucleic acid molecules encode a cytoplasmic, transmembrane, extracellular, or other domain of a polypeptide of the invention. In other embodiments, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of a nucleic acid of the invention.

Another aspect of the invention provides vectors, e.g., recombinant expression vectors, comprising a nucleic acid molecule of the invention. In another embodiment, the invention provides isolated host cells, e.g., mammalian or non-mammalian cells, containing such a vector or a nucleic acid of the invention. The invention also provides methods for producing a polypeptide of the invention by culturing, in a suitable medium, a host cell of the invention containing a recombinant expression vector encoding a polypeptide of the invention such that the polypeptide of the invention is produced.

Another aspect of this invention features isolated or recombinant proteins and polypeptides of the invention. Preferred proteins and polypeptides possess at least one biological activity possessed by the corresponding naturally-occurring human

polypeptide. An activity, a biological activity, and a functional activity of a polypeptide of the invention refers to an activity exerted by a protein or polypeptide of the invention on a responsive cell as determined in vivo, or in vitro, according to standard techniques. Such activities can be a direct activity, such as an association
5 with or an enzymatic activity exerted on a second protein or an indirect activity, such as a cellular processes mediated by interaction of the protein with a second protein.

TANGO 273 protein mediates one or more physiological responses of cells to bacterial infection, e.g., by mediating one or more of detection of bacteria in a tissue in which it is expressed, movement of cells with relation to sites of bacterial
10 infection, production of biological molecules which inhibit bacterial infection, and production of biological molecules which alleviate cellular or other physiological damage wrought by bacterial infection. TANGO 273, a transmembrane protein, is also involved in transmembrane signal transduction, and therefore mediates transmission of signals between the extracellular and intracellular environments of
15 cells. TANGO 273 mediates regulation of cell growth and proliferation, endocytosis, activation of respiratory burst, and other physiological processes triggered by transmission of a signal via a protein with which TANGO 273 interacts. The compositions and methods of the invention can therefore be used to prevent, diagnose, and treat disorders involving one or more physiological activities mediated
20 by TANGO 273 protein.

As an additional example, TANGO 325 polypeptides, nucleic acids, and modulators thereof modulate growth, proliferation, survival, differentiation, and activity of human tissues such as vascular endothelium, including aortic endothelium, other heart tissues, placenta, liver, kidney, and pancreas tissues. Thus, TANGO 325
25 polypeptides, nucleic acids, and modulators thereof can therefore be used to prevent, diagnose, and treat disorders involving one or more physiological activities mediated by TANGO 325 protein in tissues in which it is expressed. Such activities include, for example, modulation of cardiac contractility and vasomotor tone, modulation of

leukocyte extravasation, sensing physiological signals by the endocrine system, modulating growth, development, maintenance, and regeneration of neurons, and the like.

5 TANGO 364, compounds which modulate its activity, expression, or both, and compounds (e.g., antibodies) which bind with TANGO 364 (collectively "TANGO 364-related molecules") exhibit the ability to affect one or more of growth, proliferation, survival, differentiation, activity, morphology, and movement/migration of, for example, human fetal and adult skin cells and tissue. Furthermore, TANGO 364 is involved in modulating cell-to-cell adhesion, tissue and extracellular matrix invasivity of cells, 10 infectivity of cells by pathogens (e.g., bacteria and viruses), endocrine signaling processes, tissue developmental and organizational processes, and the like. Thus, TANGO 364-related molecules can be used to prognosticate, prevent, diagnose, or treat one or more disorders associated with these physiological processes.

15 TANGO 405, compounds which modulate its activity, expression, or both, and compounds (e.g., antibodies) which bind with TANGO 405 (collectively "TANGO 405-related molecules") modulate one or more of growth, proliferation, survival, differentiation, activity, morphology, and movement/migration of human lymphocytes and bone marrow cells and tissues. As described herein, TANGO 405 is involved in activation of leukocytes, including modulating one or more of growth, proliferation, survival, 20 differentiation, activity, morphology, movement/migration, and other cellular processes by which leukocytes are characterized. TANGO 405 is involved in disorders associated with aberrant activation of leukocytes, including both auto-immune disorders and disorders related to inappropriate activity or activation of leukocytes and disorders related to uncontrolled proliferation of leukocytes.

25 M019 protein, compounds which modulate its activity, expression, or both, and compounds (e.g., antibodies) which bind with M019 (collectively "M019-related molecules") exhibit the ability to affect growth, proliferation, survival, differentiation, and activity of adipose tissue cells.

In one embodiment, a polypeptide of the invention has an amino acid sequence sufficiently identical to a polypeptide of the invention or to an identified domain thereof. As used herein, the term "sufficiently identical" refers to a first amino acid or nucleotide sequence which contains a sufficient or minimum number of identical or equivalent (e.g., with a similar side chain) amino acid residues or nucleotides to a second amino acid or nucleotide sequence such that the first and second amino acid or nucleotide sequences have a common domain and/or common functional activity. For example, amino acid or nucleotide sequences which contain a common domain having about 65% identity, preferably 75% identity, more preferably 85%, 95%, or 98% identity are defined herein as sufficiently identical.

In one embodiment, the isolated polypeptide of the invention lacks both a transmembrane and a cytoplasmic domain. In another embodiment, the polypeptide lacks both a transmembrane domain and a cytoplasmic domain and is soluble under physiological conditions.

The polypeptides of the present invention, or biologically active portions thereof, can be operably linked with a heterologous amino acid sequence to form fusion proteins. The invention further features antibody substances that specifically bind a polypeptide of the invention, such as monoclonal or polyclonal antibodies, antibody fragments, and single-chain antibodies. In addition, the polypeptides of the invention or biologically active portions thereof can be incorporated into pharmaceutical compositions, which optionally include pharmaceutically acceptable carriers. These antibody substances can be made, for example, by providing the polypeptide of the invention to an immunocompetent vertebrate and thereafter harvesting blood or serum from the vertebrate.

In another aspect, the present invention provides methods for detecting the presence of the activity or expression of a polypeptide of the invention in a biological sample by contacting the biological sample with an agent capable of

detecting an indicator of activity such that the presence of activity is detected in the biological sample.

In another aspect, the invention provides methods for modulating activity of a polypeptide of the invention comprising contacting a cell with an agent that
5 modulates (inhibits or enhances) the activity or expression of a polypeptide of the invention such that activity or expression in the cell is modulated. In one embodiment, the agent is an antibody that specifically binds with a polypeptide of the invention.

In another embodiment, the agent modulates expression of a polypeptide of
10 the invention by modulating transcription, splicing, or translation of an mRNA encoding a polypeptide of the invention. In yet another embodiment, the agent is a nucleic acid molecule having a nucleotide sequence that is antisense with respect to the coding strand of an mRNA encoding a polypeptide of the invention.

The present invention also provides methods of treating a subject having a
15 disorder characterized by aberrant activity of a polypeptide of the invention or aberrant expression of a nucleic acid of the invention by administering an agent which is a modulator of the activity of a polypeptide of the invention or a modulator of the expression of a nucleic acid of the invention to the subject. In one embodiment, the modulator is a protein of the invention. In another embodiment, the
20 modulator is a nucleic acid of the invention. In other embodiments, the modulator is a peptide, peptidomimetic, or other small molecule. In yet another embodiment, the modulator is an antibody.

The present invention also provides diagnostic assays for identifying the presence or absence of a genetic lesion or mutation characterized by at least one of:
25 (i) aberrant modification or mutation of a gene encoding a polypeptide of the invention, (ii) mis-regulation of a gene encoding a polypeptide of the invention, and (iii) aberrant post-translational modification of a polypeptide of the invention

wherein a wild-type form of the gene encodes a polypeptide having the activity of the polypeptide of the invention.

In another aspect, the invention provides a method for identifying a compound that binds with or modulates the activity of a polypeptide of the invention.

- 5 In general, such methods entail measuring a biological activity of the polypeptide in the presence and absence of a test compound and identifying those compounds which bind with or alter the activity of the polypeptide.

The invention also features methods for identifying a compound which modulates the expression of a polypeptide or nucleic acid of the invention by
10 measuring the expression of the polypeptide or nucleic acid in the presence and absence of the compound.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

15 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 comprises Figures 1A through 1J. The nucleotide sequence (SEQ ID NO: 1) of a cDNA encoding the human TANGO 273 protein described herein is listed in Figures 1A-1C. The ORF (residues 135 to 650; SEQ ID NO: 2) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence
20 (SEQ ID NO: 3) of human TANGO 273 is listed. The nucleotide sequence (SEQ ID NO: 11) of a cDNA encoding the murine TANGO 273 protein described herein is listed in Figures 1D-1G. The ORF (residues 137 to 652; SEQ ID NO: 12) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 13) of murine TANGO 273 is listed. An alignment of the amino acid
25 sequences of human ("Hum."; SEQ ID NO: 3) and murine ("Mur."; SEQ ID NO: 13) TANGO 273 protein is shown in Figure 1H, wherein identical amino acid residues are indicated by ":" and similar amino acid residues are indicated by ".". Figure 1I is

a hydrophobicity plot of human TANGO 273 protein, and Figure 1J is a hydrophobicity plot of murine TANGO 273 protein.

Figure 2 comprises Figures 2A through 2M-18. The nucleotide sequence (SEQ ID NO: 21) of a cDNA encoding the human TANGO 325 protein described herein is listed in Figures 2A through 2E. The ORF (residues 135 to 2000; SEQ ID NO: 22) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 23) of human TANGO 325 is listed. Figure 2F is a hydrophobicity plot of TANGO 325 protein. An alignment of the amino acid sequences of TANGO 325 ("325"; SEQ ID NO: 23) and Slit-1 protein ("Slit"; SEQ ID NO: 29) protein is shown in Figures 2G to 2L. In Figures 2M-1 to 2M-18, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 325 protein ("325"; SEQ ID NO: 23) and the nucleotide sequence of the cDNA encoding Slit-1 protein ("Slit"; SEQ ID NO: 30) is shown. This alignment was made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4).

Figure 3 comprises Figures 3A through 3K. The nucleotide sequence (SEQ ID NO: 31) of a cDNA encoding the human TANGO 364 protein described herein is listed in Figures 3A through 3E. The ORF (residues 235 to 1764; SEQ ID NO: 32) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 33) of human TANGO 364 is listed. Figure 3F is a hydrophobicity plot of human TANGO 364 protein. The nucleotide sequence (SEQ ID NO: 41) of an alternatively-spliced form of the cDNA encoding the human TANGO 364 protein described herein is listed in Figures 3G through 3I. The ORF (residues 2 to 898; SEQ ID NO: 42) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 43) of the protein encoded by the splice variant is listed. Figures 3J and 3K are an alignment of the amino acid sequence of SEQ ID NOs: 33 and 43.

Figure 4 comprises Figures 4A through 4P. The nucleotide sequence (SEQ ID NO: 51) of a cDNA encoding the human TANGO 405 protein described herein is listed in

Figures 4A through 4C. The ORF (residues 154 to 780; SEQ ID NO: 52) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 53) of human TANGO 405 is listed. Figure 4D is a hydrophobicity plot of human TANGO 405 protein. The nucleotide sequence (SEQ ID NO: 61) of a cDNA encoding the murine

5 TANGO 405 protein described herein is listed in Figures 4E and 4F. The ORF (residues 174 to 707; SEQ ID NO: 62) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 63) of murine TANGO 405 is listed. Figure 4G is a hydrophobicity plot of murine TANGO 405 protein. An alignment of the amino acid sequences of human TANGO 405 protein (SEQ ID NO: 53) and murine TANGO 405

10 protein (SEQ ID NO: 63) amino acid sequences is shown in Figure 4H. An alignment of the nucleotide sequences of the human (SEQ ID NO: 52) and murine (SEQ ID NO: 62) ORFs encoding TANGO 405 protein is shown in Figures 4I through 4K. Figure 4L is an alignment of the amino acid sequences of murine TANGO 405 protein ("mT405"; SEQ ID NO: 63) and murine dectin-2 ("Dectin"; SEQ ID NO: 60). Figure 4M is an alignment of

15 the amino acid sequences of human TANGO 405 protein ("hT405"; SEQ ID NO: 53) and murine dectin-2 ("Dectin"; SEQ ID NO: 60). The nucleotide sequence (SEQ ID NO: 71) of an alternative embodiment of a cDNA encoding the murine TANGO 405 protein described herein is listed in Figures 4N, 4O and 4P. The ORF (residues 179 to 805; SEQ ID NO: 72) of the cDNA is indicated by nucleotide triplets, above which the amino acid

20 sequence (SEQ ID NO: 73) of the alternative embodiment of murine TANGO 405 is listed.

Figure 5 comprises Figures 5A through 5C. The nucleotide sequence (SEQ ID NO: 81) of a cDNA encoding the human M019 (i.e., TANGO 533) protein described herein is listed in Figures 5A and 5B. The ORF (residues 331 to 585; SEQ ID NO: 82) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence

25 (SEQ ID NO: 83) of human M019 protein is listed. Figure 5C is a hydrophobicity plot of human M019 protein, in which the locations of cysteine residues ("Cys"), and the predicted extracellular ("out"), intracellular ("ins"), or transmembrane ("TM") locations of the protein backbone is indicated by a horizontal bar.

DETAILED DESCRIPTION OF THE INVENTION

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The present invention is based, at least in part, on the discovery of a variety of cDNA molecules which encode proteins which are herein designated TANGO 273, TANGO 325, TANGO 364, TANGO 405, and M019. These proteins exhibit a variety of physiological activities, and are included in a single application for the sake of convenience. It is understood that the allowability or non-allowability of claims directed to one of these proteins has no bearing on the allowability of claims directed to the others. The characteristics of each of these proteins and the cDNAs encoding them are described separately in the ensuing sections. In addition to the full length mature and immature proteins described in the following sections, the invention includes fragments, derivatives, and variants of these proteins, as described herein. These proteins, fragments, derivatives, and variants are collectively referred to herein as polypeptides of the invention or proteins of the invention.

15 TANGO 273

A cDNA clone (designated jthoc028g06) encoding at least a portion of human TANGO 273 protein was isolated from a lipopolysaccharide- (LPS-)stimulated human osteoblast cDNA library. The corresponding murine cDNA clone (designated jtmoe001c04) was isolated from an LPS-stimulated murine osteoblast cDNA library.

20 The human and murine TANGO 273 proteins are predicted by structural analysis to be transmembrane proteins.

The full length of the cDNA encoding human TANGO 273 protein (Figure 1; SEQ ID NO: 1) is 2964 nucleotide residues. The ORF of this cDNA, nucleotide residues 135 to 650 of SEQ ID NO: 1 (i.e., SEQ ID NO: 2), encodes a 172-amino acid transmembrane protein (Figure 1; SEQ ID NO: 3).

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The invention thus includes purified human TANGO 273 protein, both in the form of the immature 172 amino acid residue protein (SEQ ID NO: 3) and in the form of the mature 150 amino acid residue protein (SEQ ID NO: 5). The invention also

includes purified murine TANGO 273 protein, both in the form of the immature 172 amino acid residue protein (SEQ ID NO: 13) and in the form of the mature 150 amino acid residue protein (SEQ ID NO: 15). Mature human or murine TANGO 273 proteins can be synthesized without the signal sequence polypeptide at the amino terminus thereof, or they can be synthesized by generating immature TANGO 273 protein and cleaving the signal sequence therefrom.

The invention also includes nucleic acid molecules which encode a polypeptide of the invention. Such nucleic acids include, for example, a DNA molecule having the nucleotide sequence listed in SEQ ID NO: 1 or some portion thereof or SEQ ID NO: 12 or some portion thereof, such as the portion which encodes mature TANGO 273 protein, immature TANGO 273 protein, or a domain of TANGO 273 protein. These nucleic acids are collectively referred to as nucleic acids of the invention.

TANGO 273 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features. This family includes, by way of example, the human and murine TANGO 273 proteins.

A common domain of TANGO 273 proteins is a signal sequence. As used herein, a signal sequence includes a peptide of at least about 10 amino acid residues in length which occurs at the amino terminus of membrane-bound proteins and which contains at least about 45% hydrophobic amino acid residues such as alanine, leucine, isoleucine, phenylalanine, proline, tyrosine, tryptophan, or valine. In a preferred embodiment, a signal sequence contains at least about 10 to 35 amino acid residues, preferably about 10 to 20 amino acid residues, and has at least about 35-60%, more preferably 40-50%, and more preferably at least about 45% hydrophobic residues. A signal sequence serves to direct a protein containing such a sequence to a lipid bilayer. Thus, in one embodiment, a TANGO 273 protein contains a signal sequence corresponding to amino acid residues 1 to 22 of SEQ ID NO: 3 (SEQ ID NO: 4) or to amino acid residues 1 to 22 of SEQ ID NO: 13. The signal sequence is cleaved during processing of the mature protein.

TANGO 273 proteins can also include an extracellular domain. The human TANGO 273 protein extracellular domain is located from about amino acid residue 23 to about amino acid residue 60 of SEQ ID NO: 3, and the murine TANGO 273 protein extracellular domain is located from about amino acid residue 23 to about amino acid residue 60 of SEQ ID NO: 13.

The present invention also includes TANGO 273 proteins having a transmembrane domain. As used herein, a "transmembrane domain" refers to an amino acid sequence having at least about 15 to 50 amino acid residues in length and which contains at least about 65-70% hydrophobic amino acid residues such as alanine, leucine, phenylalanine, proline, tyrosine, tryptophan, or valine. In a preferred embodiment, a transmembrane domain has at least about 60-80%, more preferably 65-75%, and more preferably at least about 70% hydrophobic residues. Thus, in one embodiment, a human TANGO 273 protein of the invention contains a transmembrane domain corresponding to about amino acid residues 61 to 81 of SEQ ID NO: 3 (SEQ ID NO: 7). In another embodiment, a murine TANGO 273 protein of the invention contains a transmembrane domain corresponding to about amino acid residues 61 to 81 of SEQ ID NO: 13.

In addition, TANGO 273 proteins include a cytoplasmic domain. The human TANGO 273 cytoplasmic domain is located from about amino acid residue 82 to amino acid residue 172 of SEQ ID NO: 3 (SEQ ID NO: 8), and the murine TANGO 273 cytoplasmic domain is located from about amino acid residue 82 to amino acid residue 172 of SEQ ID NO: 13.

TANGO 273 proteins typically comprise a variety of potential post-translational modification sites (often within an extracellular domain), such as those described herein in Tables I and II, as predicted by computerized sequence analysis of human and murine TANGO 273 proteins using amino acid sequence comparison software (comparing the amino acid sequence of TANGO 273 with the information in the PROSITE database {rel. 12.2; Feb, 1995} and the Hidden Markov Models database

{Rel. PFAM 3.3}). As used herein, the term "post-translational modification site" refers to a protein domain that includes about 3 to 10 amino acid residues, more preferably about 3 to 6 amino acid residues wherein the domain has an amino acid sequence which comprises a consensus sequence which is recognized and modified by a protein-modifying enzyme. Examples of protein-modifying enzymes include amino acid glycosylases, cAMP- and cGMP-dependent protein kinases, protein kinase C, casein kinase II, and myristoylases. In certain embodiments, a protein of the invention has at least 1, 2, 3, 4, 5, or all 6 of the post-translational modification sites listed in Table I. In other embodiments, the protein of the invention has at least 1, 2, 3, 4, 5, 6, or all 7 of the post-translational modification sites listed in Table II.

Table I

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 3	Amino Acid Sequence
N-glycosylation site	97 to 100	NVSY
Casein kinase II phosphorylation site	41 to 44	SYED
N-myristoylation site	31 to 36	GLYPTY
	47 to 52	GSRCCV
	70 to 75	GVL FCC
	131 to 136	GNSMAM
Src Homology 3 (SH3) domain binding site	86 to 90	YPPPL
	103 to 107	QPPNP
	113 to 117	QPGPP
	121 to 125	DPGGP
	140 to 145	VPPNSP
	151 to 155	CPPPP
	160 to 164	TPPPP

Table II

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 13	Amino Acid Sequence
N-glycosylation site	97 to 100	NVSY
Casein kinase II phosphorylation site	41 to 44	SYED
N-myristoylation site	31 to 36	GLYPTY
	47 to 52	GSRCCV
	70 to 75	GVL FCC
	131 to 136	GNTMAM
Src Homology 3 (SH3) domain binding site	86 to 90	YPPPL
	103 to 107	QPPNP
	115 to 119	GPPYY
	121 to 125	DPGGP
	141 to 145	QPN SP
	151 to 155	YPPPP
	160 to 164	TPPPP
Amidation site	1 to 4	MGRR

5 The amino acid sequence of TANGO 273 protein includes about seven potential proline-rich Src homology 3 (SH3) domain binding sites nearer the cytoplasmic portion of the protein. SH3 domains mediate specific assembly of protein complexes, presumably by interacting with proline-rich protein domains (Morton and Campbell (1994) Curr. Biol. 4:615-617). SH3 domains also mediate interactions between proteins involved in transmembrane signal transduction. Coupling of proteins mediated by SH3 domains has been implicated in a variety of physiological systems, including those involving regulation of cell growth and proliferation, endocytosis, and activation of respiratory burst.

10

SH3 domains have been described in the art (e.g., Mayer et al. (1988) Nature 332:272-275; Musacchio et al. (1992) FEBS Lett. 307:55-61; Pawson and Schlessinger (1993) Curr. Biol. 3:434-442; Mayer and Baltimore (1993) Trends Cell Biol. 3:8-13; Pawson (1993) Nature 373:573-580), and occur in a variety of cytoplasmic proteins, including several (e.g., protein tyrosine kinases) involved in transmembrane signal transduction. Among the proteins in which one or more SH3 domains occur are protein tyrosine kinases such as those of the Src, Abl, Bkt, Csk and ZAP70 families, mammalian phosphatidylinositol-specific phospholipases C-gamma-1 and -2, mammalian phosphatidylinositol 3-kinase regulatory p85 subunit, mammalian Ras GTPase-activating protein (GAP), proteins which mediate binding of guanine nucleotide exchange factors and growth factor receptors (e.g., vertebrate GRB2, *Caenorhabditis elegans* sem-5, and *Drosophila* DRK proteins), mammalian Vav oncoprotein, guanidine nucleotide releasing factors of the CDC 25 family (e.g., yeast CDC25, yeast SCD25, and fission yeast ste6 proteins), MAGUK proteins (e.g., mammalian tight junction protein ZO-1, vertebrate erythrocyte membrane protein p55, *C. elegans* protein lin-2, rat protein CASK, and mammalian synaptic proteins SAP90/PSD-95, CHAPSYN-110/PSD-93, SAP97/DLG1, and SAP102), proteins which interact with vertebrate receptor protein tyrosine kinases (e.g., mammalian cytoplasmic protein Nck and oncoprotein Crk), chicken Src substrate p80/85 protein (cortactin), human hemopoietic lineage cell specific protein Hs1, mammalian dihydropyridine-sensitive L-type calcium channel beta subunit, human myasthenic syndrome antigen B (MSYB), mammalian neutrophil cytosolic activators of NADPH oxidase (e.g., p47 {NCF-1}, p67 {NCF-2}, and *C. elegans* protein B0303.7) myosin heavy chains (MYO3) from amoebae, from slime molds, and from yeast, vertebrate and *Drosophila* spectrin and fodrin alpha chain proteins, human amphiphysin, yeast actin-binding proteins ABP1 and SLA3, yeast protein BEM1, fission yeast protein scd2 (ral3), yeast BEM1-binding proteins BOI2 (BEB1) and BOB1 (BOI1), yeast fusion protein FUS1, yeast protein RSV167, yeast protein SSU81, yeast hypothetical proteins

YAR014c, YFR024c, YHL002w, YHR016c, YJL020C, and YHR114w, hypothetical fission yeast protein SpAC12C2.05c, and *C. elegans* hypothetical protein F42H10.3.

Of these proteins, multiple SH3 domains occur in vertebrate GRB2 protein, *C. elegans* sem-5 protein, *Drosophila* DRK protein, oncoprotein Crk, mammalian neutrophil

5 cytosolic activators of NADPH oxidase p47 and p67, yeast protein BEM1, fission yeast protein scd2, yeast hypothetical protein YHR114w, mammalian cytoplasmic protein Nck, *C. elegans* neutrophil cytosolic activator of NADPH oxidase B0303.7, and yeast actin-binding protein SLA1. Of these proteins, three or more SH3 domains occur in
10 mammalian cytoplasmic protein Nck, *C. elegans* neutrophil cytosolic activator of NADPH oxidase B0303.7, and yeast actin-binding protein SLA1. The presence of SH3 domain binding sites in TANGO 273 indicates that TANGO 273 interacts with one or more of these and other SH3 domain-containing proteins and is thus involved in physiological processes in which one or more of these or other SH3 domain-containing proteins are involved.

15 The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that human TANGO 273 protein includes a 22 amino acid signal peptide (amino acid residues 1 to 22 of SEQ ID NO: 3; SEQ ID NO: 4) preceding the mature TANGO 273 protein (amino acid residues 23 to 172 of SEQ ID NO: 3; SEQ ID NO: 5). Human TANGO 273 protein includes an extracellular domain
20 (amino acid residues 23 to 60 of SEQ ID NO: 3; SEQ ID NO: 6); a transmembrane domain (amino acid residues 61 to 81 of SEQ ID NO: 3; SEQ ID NO: 7); and a cytoplasmic domain (amino acid residues 82 to 172 of SEQ ID NO: 3; SEQ ID NO: 8).

Figure 1I depicts a hydrophobicity plot of human TANGO 273 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively
25 hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 3 is the signal sequence of human TANGO 273 (SEQ ID NO: 4). The hydrophobic region which corresponds to amino acid residues 61 to 81 of SEQ ID NO: 3 is the transmembrane

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domain of human TANGO 273 (SEQ ID NO: 7). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 273 protein from about amino acid residue 100 to about amino acid residue 120 appears to be located at or near the surface of the protein, while the region from about amino acid residue 130 to about amino acid residue 140 appears not to be located at or near the surface.

Chromosomal mapping was performed by computerized comparison of TANGO 273 cDNA sequences against a chromosomal mapping database in order to identify the approximate location of the gene encoding human TANGO 273 protein. This analysis indicated that the gene is located on chromosome 7 between markers D7S2467 and D7S2552.

The predicted molecular weight of human TANGO 273 protein without modification and prior to cleavage of the signal sequence is about 19.2 kilodaltons. The predicted molecular weight of the mature human TANGO 273 protein without modification and after cleavage of the signal sequence is about 16.8 kilodaltons.

Northern analysis experiments indicated that mRNA corresponding to the cDNA encoding TANGO 273 is expressed in the tissues listed in Table III, wherein "++" indicates moderate expression and "+" indicates lower expression.

Table III

Animal	Tissue	Relative Level of Expression
Human	heart	++
	brain	++
	skeletal muscle	++
	pancreas	++
	placenta	+
	lung	+
	liver	+
	kidney	+

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The full length of the cDNA encoding murine TANGO 273 protein (Figure 1; SEQ ID NO: 11) is 2915 nucleotide residues. The ORF of this cDNA, nucleotide residues 137 to 650 of SEQ ID NO: 11 (i.e., SEQ ID NO: 12), encodes a 172-amino acid transmembrane protein (Figure 1; SEQ ID NO: 13).

5 The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that murine TANGO 273 protein includes a 22 amino acid signal peptide (amino acid residues 1 to 22 of SEQ ID NO: 13) preceding the mature TANGO 273 protein (amino acid residues 23 to 172 of SEQ ID NO: 13; SEQ ID NO: 15). Murine TANGO 273 protein includes an extracellular domain (amino acid residues 23 to 60 of SEQ ID NO: 13); a transmembrane domain (amino acid residues 61 to 81 of SEQ ID NO: 13); and a cytoplasmic domain (amino acid residues 82 to 172 of SEQ ID NO: 13).

10 Figure 1J depicts a hydrophobicity plot of murine TANGO 273 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 13 is the signal sequence of murine TANGO 273. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 273 protein from about amino acid residue 100 to about amino acid residue 120 appears to be located at or near the surface of the protein, while the region from about amino acid residue 130 to about amino acid residue 140 appears not to be located at or near the surface.

15 The predicted molecular weight of murine TANGO 273 protein without modification and prior to cleavage of the signal sequence is about 19.4 kilodaltons. The predicted molecular weight of the mature murine TANGO 273 protein without modification and after cleavage of the signal sequence is about 17.1 kilodaltons.

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In situ analysis of murine TANGO 273 mRNA indicated that TANGO 273 is expressed in central nervous system (CNS) tissues during embryogenesis and into adulthood. Expression of TANGO 273 is widely observed in murine CNS tissues, including brain, spinal cord, eye, and olfactory epithelium at all embryonic ages examined (i.e., at embryonic days 13.5, 14.5, 15.5, 16.5, and 18.5 and at post-natal day 1.5).

Human and murine TANGO 273 cDNA sequences exhibit significant nucleotide sequence identity with an expressed sequence tag (EST) isolated from a library of ESTs corresponding to proteins secreted from prostate tissue, as described in PCT publication number WO 99/06550, published February 11, 1999.

Human and murine TANGO 273 proteins exhibit considerable sequence similarity, as indicated herein in Figure 1H. Figure 1H depicts an alignment of human and murine TANGO 273 protein amino acid sequences (SEQ ID NOs: 3 and 13, respectively). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the proteins are 89.5% identical. Alignment of the ORF encoding human TANGO 273 protein and the ORF encoding murine TANGO 273 protein using the same software and parameters indicated that the nucleotide sequences are 84.1% identical.

Uses of TANGO 273 Nucleic acids,
Polypeptides, and Modulators Thereof

cDNAs encoding the human and murine TANGO 273 proteins were each isolated from LPS-stimulated osteoblast cDNA libraries. These proteins are involved in bone-related metabolism, homeostasis, and development disorders. Thus, proteins and nucleic acids of the invention which are identical to, similar to, or derived from human and murine TANGO 273 proteins and nucleic acids encoding them are useful for preventing, diagnosing, and treating, among others, bone-related disorders such as osteoporosis, cancer, skeletal development disorders, bone fragility, and the like.

Expression of TANGO 273 in heart, brain, skeletal muscle, and pancreas, placenta, lung, liver, and kidney tissues is an indication that TANGO 273 proteins, nucleic acids encoding them, and agents that modulate activity or expression of either of these can be used to modulate growth, proliferation, survival, differentiation, adhesion, and activity of cells of these tissues, or to prognosticate, diagnose, and treat one or more disorders which affect these tissues.

The fact that TANGO 273 is expressed at high levels in neurological tissues is an indication that TANGO 273 proteins, nucleic acids, and modulators thereof can be used to modulate proliferation, differentiation, or function of neurological cells in these tissues (e.g., neuronal cells). Thus, TANGO 273 proteins, nucleic acids, and modulators thereof can be used to prognosticate, diagnose, and treat one or more neurological disorders. Examples of such disorders include CNS disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders, and other neurological and cerebrovascular disorders.

CNS disorders include, but are not limited to cognitive and neurodegenerative disorders such as Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, and Parkinson's disease, as well as Gilles de la Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders (e.g., insomnia, hypersomnia, parasomnia, and sleep apnea); neuropsychiatric disorders (e.g., schizophrenia, schizoaffective disorder, attention deficit disorder, dysthymic disorder, major depressive disorder, mania, and obsessive-compulsive disorder); psychoactive substance use disorders; anxiety; panic disorder; and bipolar affective disorders (e.g., severe bipolar affective disorder and bipolar affective disorder with hypomania and major depression).

CNS-related disorders include disorders associated with developmental, cognitive, and autonomic neural and neurological processes, such as pain, appetite, long term memory, and short term memory.

5 Examples of focal brain disorders include aphasia, apraxia, agnosia, and amnesias (e.g., posttraumatic amnesia, transient global amnesia, and psychogenic amnesia). Global-diffuse cerebral disorders with which TANGO 273 can be associated include coma, stupor, obtundation, and disorders of the reticular formation.

10 Other neurological disorders with which TANGO 273 can be associated include ischemic syndromes (e.g., stroke), hypertensive encephalopathy, hemorrhagic disorders, and disorders involving aberrant function of the blood-brain barrier (e.g., CNS infections such as meningitis and encephalitis, aseptic meningitis, metastasis of non-CNS tumor cells into the CNS, various pain disorders such as migraine, blindness and other vision problems, and CNS-related adverse drug reactions such as head pain, sleepiness, and confusion). TANGO 273 proteins, nucleic acids encoding them, and agents that modulate activity or expression of either of these can be used to prognosticate, diagnose, and treat one or more of these disorders.

15 Developmental regulation of TANGO 273 expression in fetal neurological tissues, as described herein, is an indication that TANGO 273 proteins, nucleic acids, and modulators thereof can be used to prognosticate, diagnose, and treat one or more disorders which involve aberrant fetal neurological development. Examples of such disorders include blindness, deafness, fetal death, mental retardation, dysraphia, anencephaly, malformation of cerebral hemispheres, encephalocele, porencephaly, hydranencephaly, hydrocephalus, and spina bifida.

20 The fact that TANGO 273 is expressed in tissues which were exposed to LPS indicates that TANGO 273 mediates one or more physiological responses of cells to bacterial infection. Thus, TANGO 273 is involved in one or more of detection of bacteria in a tissue in which it is expressed, movement of cells with relation to sites of bacterial infection, production of biological molecules which inhibit bacterial infection,

and production of biological molecules which alleviate cellular or other physiological damage wrought by bacterial infection.

Presence in TANGO 273 protein of multiple SH3 domain binding sites indicates that TANGO 273 protein interacts with one or more SH3 domain-
5 containing proteins. Thus, TANGO 273 protein mediates binding of proteins (i.e., binding of proteins to TANGO 273 and to one another to form protein complexes) in cells in which it is expressed. TANGO 273 is also involved in transduction of signals between the exterior environment of cells (i.e., including from other cells) and the interior of cells in which it is expressed. TANGO 273 mediates regulation of cell
10 growth and proliferation, endocytosis, activation of respiratory burst, and other physiological processes triggered by transmission of a signal via a protein with which TANGO 273 interacts.

Sequence similarity of TANGO 273 cDNA with an EST expressed in prostate tissue indicates that TANGO 273 can be expressed in prostate tissue, and can thus be
15 involved in disorders of the prostate. Thus, TANGO 273 proteins, nucleic acids encoding them, and agents that modulate activity or expression of either of these can be used to treat prostate disorders. Examples of prostate disorders which can be treated in this manner include inflammatory prostatic diseases (e.g., acute and chronic prostatitis and granulomatous prostatitis), prostatic hyperplasia (e.g., benign prostatic hypertrophy or hyperplasia), and prostate tumors (e.g., carcinomas).
20

In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat cardiovascular disorders. Examples of cardiac disorders which can be treated in this manner include ischemic heart diseases (e.g., angina pectoris, myocardial infarction and its aftermath, coronary artery disease, cardiac
25 arrest, and chronic ischemic heart disease), hypertensive heart disease, pulmonary heart disease, valvular heart disease (e.g., rheumatic fever and rheumatic heart disease, endocarditis, mitral valve prolapse, and aortic valve stenosis), congenital heart disease (e.g., valvular and vascular obstructive lesions, atrial or ventricular septal defect, and

patent ductus arteriosus), cardiac arrhythmia, cardiac insufficiency, endocarditis, pericardial disease, muscular dystrophy, and myocardial disease (e.g., myocarditis, congestive cardiomyopathy, restrictive cardiomyopathy, and hypertrophic cardiomyopathy). Examples of vascular disorders which can be treated in this manner

5 include arteriosclerosis, atherosclerosis, hypertension, aberrant or non-desired angiogenesis, stenosis and restenosis, and smooth muscle proliferation in response to traumatic injury.

In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat disorders of the brain. Examples of brain disorders in

10 which TANGO 273 can have role include both CNS disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders, and other neurological and cerebrovascular disorders. CNS disorders include, but are not limited to cognitive and neurodegenerative disorders such as Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, and Parkinson's disease, as well as Gilles de la

15 Tourette's syndrome, autonomic function disorders such as hypertension and sleep disorders (e.g., insomnia, hypersomnia, parasomnia, and sleep apnea), neuropsychiatric disorders (e.g., schizophrenia, schizoaffective disorder, attention deficit disorder, dysthymic disorder, major depressive disorder, mania, and obsessive-compulsive disorder), psychoactive substance use disorders, anxiety, panic disorder, and bipolar

20 affective disorder (e.g., severe bipolar affective disorder and bipolar affective disorder with hypomania and major depression). CNS-related disorders include disorders associated with developmental, cognitive, and autonomic neural and neurological processes, such as pain, appetite, long term memory, and short term memory.

Examples of focal brain disorders include aphasia, apraxia, agnosia, and amnesias (e.g.,

25 posttraumatic amnesia, transient global amnesia, and psychogenic amnesia). Global-diffuse cerebral disorders with which TANGO 273 is associated include coma, stupor, obtundation, and disorders of the reticular formation. Cerebrovascular disorders include ischemic syndromes (e.g., stroke), hypertensive encephalopathy, hemorrhagic

disorders, and disorders involving aberrant function of the blood-brain barrier (e.g., CNS infections such as meningitis and encephalitis, aseptic meningitis, metastasis of non-CNS tumor cells into the CNS, various pain disorders such as migraine, and CNS-related adverse drug reactions such as head pain, sleepiness, and confusion).

5 In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat disorders of skeletal muscle, such as muscular dystrophy (e.g., Duchenne muscular dystrophy, Becker muscular dystrophy, Emery-Dreifuss muscular dystrophy, limb-girdle muscular dystrophy, facioscapulohumeral muscular dystrophy, myotonic dystrophy, oculopharyngeal muscular dystrophy, distal muscular
10 dystrophy, and congenital muscular dystrophy), motor neuron diseases (e.g., amyotrophic lateral sclerosis, infantile progressive spinal muscular atrophy, intermediate spinal muscular atrophy, spinal bulbar muscular atrophy, and adult spinal muscular atrophy), myopathies (e.g., inflammatory myopathies such as dermatomyositis and polymyositis, myotonia congenita, paramyotonia congenita,
15 central core disease, nemaline myopathy, myotubular myopathy, and periodic paralysis), and metabolic diseases of muscle (e.g., phosphorylase deficiency, acid maltase deficiency, phosphofructokinase deficiency, debrancher enzyme deficiency, mitochondrial myopathy, carnitine deficiency, carnitine palmityl transferase deficiency, phosphoglycerate kinase deficiency, phosphoglycerate mutase deficiency, lactate
20 dehydrogenase deficiency, and myoadenylate deaminase deficiency).

 In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat pancreatic disorders, such as pancreatitis (e.g., acute hemorrhagic pancreatitis and chronic pancreatitis), pancreatic cysts (e.g., congenital cysts, pseudocysts, and benign or malignant neoplastic cysts), pancreatic tumors (e.g.,
25 pancreatic carcinoma and adenoma), diabetes mellitus (e.g., insulin- and non-insulin-dependent types, impaired glucose tolerance, and gestational diabetes), or islet cell tumors (e.g., insulinomas, adenomas, Zollinger-Ellison syndrome, glucagonomas, and somatostatinoma).

In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat placental disorders, such as toxemia of pregnancy (e.g., preeclampsia and eclampsia), placentitis, or spontaneous abortion.

5 In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat pulmonary disorders, such as atelectasis, cystic fibrosis, rheumatoid lung disease, pulmonary congestion or edema, chronic obstructive airway disease (e.g., emphysema, chronic bronchitis, bronchial asthma, and bronchiectasis), diffuse interstitial diseases (e.g., sarcoidosis, pneumoconiosis, hypersensitivity pneumonitis, Goodpasture's syndrome, idiopathic pulmonary hemosiderosis, pulmonary alveolar proteinosis, desquamative interstitial pneumonitis, chronic
10 interstitial pneumonia, fibrosing alveolitis, hamman-rich syndrome, pulmonary eosinophilia, diffuse interstitial fibrosis, Wegener's granulomatosis, lymphomatoid granulomatosis, and lipid pneumonia), or tumors (e.g., bronchogenic carcinoma, bronchioalveolar carcinoma, bronchial carcinoid, hamartoma, and mesenchymal tumors).
15

In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat hepatic (liver) disorders, such as jaundice, hepatic failure, hereditary hyperbilirubinemias (e.g., Gilbert's syndrome, Crigler-Naijar syndromes, and Dubin-Johnson and Rotor's syndromes), hepatic circulatory disorders (e.g., hepatic
20 vein thrombosis and portal vein obstruction and thrombosis) hepatitis (e.g., chronic active hepatitis, acute viral hepatitis, and toxic and drug-induced hepatitis) cirrhosis (e.g., alcoholic cirrhosis, biliary cirrhosis, and hemochromatosis), or malignant tumors (e.g., primary carcinoma, hepatoblastoma, and angiosarcoma).

25 In another example, TANGO 273 polypeptides, nucleic acids, or modulators thereof, can be used to treat renal (kidney) disorders, such as glomerular diseases (e.g., acute and chronic glomerulonephritis, rapidly progressive glomerulonephritis, nephrotic syndrome, focal proliferative glomerulonephritis, glomerular lesions associated with systemic disease such as systemic lupus erythematosus, Goodpasture's

syndrome, multiple myeloma, diabetes, neoplasia, sickle cell disease, and chronic inflammatory diseases), tubular diseases (e.g., acute tubular necrosis and acute renal failure, polycystic renal disease, medullary sponge kidney, medullary cystic disease, nephrogenic diabetes, and renal tubular acidosis), tubulointerstitial diseases (e.g.,
5 pyelonephritis, drug and toxin induced tubulointerstitial nephritis, hypercalcemic nephropathy, and hypokalemic nephropathy) acute and rapidly progressive renal failure, chronic renal failure, nephrolithiasis, vascular diseases (e.g., hypertension and nephrosclerosis, microangiopathic hemolytic anemia, atheroembolic renal disease, diffuse cortical necrosis, and renal infarcts), or tumors (e.g., renal cell carcinoma and
10 nephroblastoma).

TANGO 325

A cDNA clone (designated jthdc071a12) encoding at least a portion of human TANGO 325 protein was isolated from a human aortic endothelial cell cDNA library.
15 The human TANGO 325 protein is predicted by structural analysis to be a transmembrane protein.

The full length of the cDNA encoding human TANGO 325 protein (Figure 2; SEQ ID NO: 21) is 2169 nucleotide residues. The ORF of this cDNA, nucleotide residues 135 to 2000 of SEQ ID NO: 21 (i.e., SEQ ID NO: 22), encodes a 622-amino
20 acid transmembrane protein (Figure 2; SEQ ID NO: 23).

The invention thus includes purified human TANGO 325 protein, both in the form of the immature 622 amino acid residue protein (SEQ ID NO: 23) and in the form of the mature, approximately 591 amino acid residue protein (SEQ ID NO: 25). Mature human TANGO 325 protein can be synthesized without the signal sequence
25 polypeptide at the amino terminus thereof, or it can be synthesized by generating immature TANGO 325 protein and cleaving the signal sequence therefrom.

The invention also includes nucleic acid molecules which encode a TANGO 325 polypeptide of the invention. Such nucleic acids include, for example, a DNA

molecule having the nucleotide sequence listed in SEQ ID NO: 21 or some portion thereof, such as the portion which encodes mature TANGO 325 protein, immature TANGO 325 protein, or a domain of TANGO 325 protein. These nucleic acids are collectively referred to as TANGO 325 nucleic acids of the invention.

5 TANGO 325 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features.

A common domain present in TANGO 325 proteins is a signal sequence. In one embodiment, a TANGO 325 protein contains a signal sequence corresponding to about amino acid residues 1 to 31 of SEQ ID NO: 23 (SEQ ID NO: 24). The signal
10 sequence is cleaved during processing of the mature protein.

TANGO 325 proteins can include an extracellular domain. The human TANGO 325 protein extracellular domain is located from about amino acid residue 32 to about amino acid residue 529 of SEQ ID NO: 23 (SEQ ID NO: 26).

In addition, TANGO 325 include a transmembrane domain. In one
15 embodiment, a TANGO 325 protein of the invention contains a transmembrane domain corresponding to about amino acid residues 530 to 547 of SEQ ID NO: 23 (SEQ ID NO: 27).

The present invention includes TANGO 325 proteins having a cytoplasmic domain, particularly including proteins having a carboxyl-terminal cytoplasmic
20 domain. The human TANGO 325 cytoplasmic domain is located from about amino acid residue 548 to amino acid residue 622 of SEQ ID NO: 23 (SEQ ID NO: 28).

TANGO 325 proteins typically comprise a variety of potential post-translational modification sites (often within an extracellular domain), such as those described herein in Table IV, as predicted by computerized sequence analysis of
25 TANGO 325 proteins using amino acid sequence comparison software (comparing the amino acid sequence of TANGO 325 with the information in the PROSITE database {rel. 12.2; Feb, 1995} and the Hidden Markov Models database {Rel. PFAM 3.3}). In

certain embodiments, a protein of the invention has at least 1, 2, 4, 6, 10, 15, or 20 or more of the post-translational modification sites listed in Table IV.

Table IV

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 23	Amino Acid Sequence
N-glycosylation site	71 to 74	NISY
	76 to 79	NESE
	215 to 218	NLTK
	266 to 269	NVTR
	317 to 320	NDTF
	331 to 334	NLSF
	336 to 339	NLTA
	400 to 403	NITN
	410 to 413	NVSR
	451 to 454	NITF
	579 to 582	NVTA
cAMP- or cGMP-dependent protein kinase phosphorylation site	231 to 234	RRLS
Protein kinase C phosphorylation site	40 to 42	TGR
	229 to 231	SLR
	326 to 328	SLK
	390 to 392	SMR
	510 to 512	SGK
	575 to 577	SAR
Casein kinase II phosphorylation site	284 to 287	SHND
	442 to 445	SPLE
	447 to 450	TETE
	453 to 456	TFWE

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Table IV

N-myristoylation site	3 to 8	GLQFSL
	69 to 74	GNNISY
	126 to 131	GIFKGL
	174 to 179	GTFVGM
ATP/GTP-binding site motif A (P-loop)	506 to 513	AASMSGKT
Leucine rich repeat amino terminal domain (LLRNT)	32 to 60	See Fig. 2
Leucine rich repeat (LRR) domain	61 to 84	See Fig. 2
	85 to 108	See Fig. 2
	109 to 132	See Fig. 2
	133 to 156	See Fig. 2
	157 to 180	See Fig. 2
	181 to 204	See Fig. 2
	205 to 228	See Fig. 2
	229 to 252	See Fig. 2
	253 to 276	See Fig. 2
	277 to 300	See Fig. 2
	301 to 324	See Fig. 2
	326 to 349	See Fig. 2
Leucine rich repeat carboxyl terminal domain (LRRCT)	359 to 405	See Fig. 2

Among the domains that occur in TANGO 325 protein are leucine rich repeat (LRR) domains, including amino terminal and carboxyl terminal LRR domains, and a P-loop domain. In one embodiment, the protein of the invention has at least one domain that is at least 55%, preferably at least about 65%, more preferably at least about 75%, yet more preferably at least about 85%, and most preferably at least about

95% identical to one of these domains. In another embodiment, the protein has at least one amino terminal LRR domain, at least one carboxyl terminal LRR domain, and a plurality of LRR domains interposed therebetween. In yet another embodiment, the protein has at least one P-loop domain, and a plurality (e.g., 2, 3, 4, or more) of the LRR domains described herein in Table IV.

One or more LRR domains is present in a variety of proteins involved in protein-protein interactions. Such proteins include, for example, proteins involved in signal transduction, cell-to-cell adhesion, cell-to-extracellular matrix adhesion, cell development, DNA repair, RNA processing, and cellular molecular recognition processes. Specialized LRR domains, designated LRR amino terminal (LRRNT) domains and LRR carboxyl terminal (LRRCT) domains often occur near the amino and carboxyl, respectively, ends of a series of LRR domains. TANGO 325 protein has fourteen clustered LRR domains, including (from the amino terminus toward the carboxyl terminus of TANGO 325) an LRRNT domain, twelve LRR domains, and an LRRCT domain. TANGO 325 is thus involved in one or more physiological processes in which these other LRR domain-containing proteins are involved, namely binding of cells with extracellular proteins such as soluble extracellular proteins and cell surface proteins of other cells.

The fact that TANGO 325 has an ATP/GTP-binding domain (i.e., a P-loop domain) within the extracellular domain of the protein indicates that this protein is involved in transmembrane signaling events. Considered in combination with the protein-binding LRR domains present in the extracellular domain of TANGO 325 protein, the presence of the ATP/GTP-binding domain indicates that TANGO 325 protein is capable of sensing extracellular proteins, including ATP-binding proteins and GTP-binding proteins, and extracellular nucleotides (e.g., ATP, ADP, and AMP). Thus, TANGO 325 protein is involved in translating information (e.g., environmental conditions or signaling molecules provided to the environment by other cells) from the

extracellular environment of the cell in which it is expressed to one or more intracellular biochemical systems.

TANGO 325 exhibits amino acid sequence and nucleic acid sequence homology with human Slit-1 protein. An alignment of the amino acid sequences of TANGO 325 and human Slit-1 protein is shown in Figures 2G to 2L. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are 35.4% identical (i.e., 35.4% of the residues of TANGO 325 correspond to identical residues in Slit-1). An alignment of the nucleotide sequences of the ORFs encoding TANGO 325 and human Slit-1 protein is shown in Figures 2M-1 through 2M-18. The two ORFs are 65.7% identical, as assessed using the same software and parameters.

The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that human TANGO 325 protein includes an approximately 31 (i.e., 29, 30, 31, 32, or 33) amino acid residue signal peptide (amino acid residues 1 to 31 of SEQ ID NO: 23; SEQ ID NO: 24) preceding the mature TANGO 325 protein (i.e., approximately amino acid residues 42 to 622 of SEQ ID NO: 23; SEQ ID NO: 25). In one embodiment, human TANGO 325 protein includes an extracellular domain (amino acid residues 32 to 529 of SEQ ID NO: 23; SEQ ID NO: 26); a transmembrane domain (amino acid residues 530 to 547 of SEQ ID NO: 23; SEQ ID NO: 27); and a cytoplasmic domain (amino acid residues 548 to 622 of SEQ ID NO: 23; SEQ ID NO: 28). In an alternative embodiment, human TANGO 325 protein includes a cytoplasmic domain (amino acid residues 32 to 529 of SEQ ID NO: 23; SEQ ID NO: 26); a transmembrane domain (amino acid residues 530 to 547 of SEQ ID NO: 23; SEQ ID NO: 27); and an extracellular domain (amino acid residues 548 to 622 of SEQ ID NO: 23; SEQ ID NO: 28).

Figure 2F depicts a hydrophobicity plot of human TANGO 325 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively

hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 31 of SEQ ID NO: 23 is the signal sequence of human TANGO 325 (SEQ ID NO: 24). The hydrophobic region which corresponds to amino acid residues 530 to 547 of SEQ ID NO: 23 is the

5 transmembrane domain of human TANGO 325 (SEQ ID NO: 27). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 325 protein from about amino acid residue 550 to about amino acid residue 565 appears to

10 be located at or near the surface of the protein, while the region from about amino acid residue 168 to about amino acid residue 185 appears not to be located at or near the surface.

The predicted molecular weight of human TANGO 325 protein without modification and prior to cleavage of the signal sequence is about 70.3 kilodaltons.

15 The predicted molecular weight of the mature human TANGO 325 protein without modification and after cleavage of the signal sequence is about 66.8 kilodaltons.

Northern analysis experiments indicated that mRNA corresponding to the cDNA encoding TANGO 325 is expressed in the tissues listed in Table V, wherein "+" indicates expression and "-" indicates that expression could not be detected in the

20 corresponding tissue.

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TANGO 325

Table V

Animal	Tissue	Relative Level of Expression
Human	placenta	+
	liver	+
	kidney	+
	pancreas	+
	heart	+
	brain	-
	skeletal muscle	-
	lung	-

Uses of TANGO 325 Nucleic acids,
Polypeptides, and Modulators Thereof

5 TANGO 325 proteins are involved in disorders which affect both tissues in
which they are normally expressed and tissues in which they are normally not
expressed. Based on the observation that TANGO 325 is expressed in human aortic
endothelial tissue and in placenta, liver, kidney, pancreas, and heart tissues, TANGO
325 protein is involved in one or more biological processes which occur in these
10 tissues. In particular, TANGO 325 is involved in modulating growth, proliferation,
survival, differentiation, and activity of endothelial cells including, but not limited to,
vascular and cardiac (including valvular) endothelial cells of the animal in which it is
normally expressed. TANGO 325 also modulates growth, proliferation, survival,
differentiation, and activity of placenta, liver, kidney, and pancreas cells. Thus,
15 TANGO 325 has a role in disorders which affect these cells and their growth,
proliferation, survival, differentiation, and activity. TANGO 325 polypeptides, nucleic
acids, or modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or
alleviate one or more of these disorders.

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5 In one example, TANGO 325 polypeptides, nucleic acids, and modulators thereof can be used to treat placental disorders, such as the placental disorders described elsewhere in this disclosure. TANGO 325 polypeptides, nucleic acids, or modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or alleviate one or more of these disorders.

10 In another example, TANGO 325 polypeptides, nucleic acids, and modulators thereof, can be used to treat hepatic (i.e., liver) disorders, such as the hepatic disorders described elsewhere in this disclosure. TANGO 325 polypeptides, nucleic acids, or modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or alleviate one or more of these disorders.

15 In another example, TANGO 325 polypeptides, nucleic acids, or modulators thereof, can be used to treat renal (i.e., kidney) disorders, such as glomerular diseases (e.g., acute and chronic glomerulonephritis, rapidly progressive glomerulonephritis, nephrotic syndrome, focal proliferative glomerulonephritis, glomerular lesions associated with systemic disease, such as systemic lupus erythematosus, Goodpasture's syndrome, multiple myeloma, diabetes, neoplasia, sickle cell disease, and chronic inflammatory diseases), tubular diseases (e.g., acute tubular necrosis and acute renal failure, polycystic renal disease, medullary sponge kidney, medullary cystic disease, nephrogenic diabetes, and renal tubular acidosis), tubulointerstitial diseases (e.g.,
20 pyelonephritis, drug and toxin induced tubulointerstitial nephritis, hypercalcemic nephropathy, and hypokalemic nephropathy) acute and rapidly progressive renal failure, chronic renal failure, nephrolithiasis, vascular diseases (e.g., hypertension and nephrosclerosis, microangiopathic hemolytic anemia, atheroembolic renal disease, diffuse cortical necrosis, and renal infarcts), and tumors (e.g., renal cell carcinoma and
25 nephroblastoma). TANGO 325 polypeptides, nucleic acids, or modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or alleviate one or more of these disorders.

Pancreatic disorders in which TANGO 325 can be involved include the pancreatic disorders described elsewhere in this disclosure. TANGO 325 polypeptides, nucleic acids, or modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or alleviate one or more of these disorders.

5 Because TANGO 325 exhibits expression in the heart, TANGO 325 nucleic acids, proteins, and modulators thereof can be used to treat cardiovascular disorders. Examples of heart disorders with which TANGO 325 can be involved include the cardiovascular disorders described elsewhere in this disclosure. TANGO 325 polypeptides, nucleic acids, or modulators thereof can be used to prognosticate,
10 diagnose, inhibit, prevent, or alleviate one or more of these disorders.

 It is known that serum nucleotide levels (e.g., ATP) affect cardiac contractility and vasomotor tone. Presence in TANGO 325 of an ATP/GTP binding domain in the extracellular portion thereof implicates this transmembrane protein in sensing of serum nucleotide levels and transmission of the sensed level by mechanisms not yet fully
15 understood to myocytes underlying the epithelium. Thus, TANGO 325 is involved in disorders such as cardiovascular insufficiency, hypertension, hypotension, shock, and the like.

 Leukocytes are known to bind with vascular endothelial surfaces in a reversible manner prior to penetrating the vascular endothelium in route to an underlying tissue.
20 Although a few proteins have previously been implicated in the leukocyte-endothelium binding process, the identities of all of the proteins involved remain unknown. The presence of numerous LRR domains on the exterior portion of TANGO 325 protein implicates this protein in reversible binding of leukocytes to vascular endothelium. Thus, TANGO 325 is involved in physiological processes and disorders which involve
25 leukocyte-endothelium binding. Such processes and disorders include, by way of example, cellular aspects of immune responses, autoimmune responses and disorders, and migration of leukocytes to lymph nodes.

5 The aortic endothelium, as well as other vascular endothelia, are known to be involved in detection of signals (e.g., metabolites, proteins, and the like) in the blood stream. Mammalian Slit-1 protein is known to be involved in the human endocrine system (Itoh et al. (1998) Brain Res. Mol. Brain Res. 62:175-186). Amino acid and nucleic acid sequence similarity of TANGO 325 with human Slit-1 protein, as described herein, indicates that TANGO 325 is involved in sensing physiological signals by the endocrine system. Thus, TANGO 325 is involved in one or more human endocrine disorders such as pituitary disorders (e.g., diabetes insipidus), thyroid disorders (e.g., hyperthyroidism, hypothyroidism, diabetes, goiter, and growth and developmental disorders), adrenal disorders (e.g., Addison's disease, Cushing's syndrome, hyperaldosteronism, and pheochromocytoma), and the like.

10 Human Slit-1 protein is also known to be involved in guidance of neuronal growth. The sequence similarity of TANGO 325 with Slit-1, as described herein, implicates TANGO 325 in growth, development, maintenance, and regeneration of neurons. TANGO 325 can thus be used to prevent, diagnose, and treat a variety of neurological disorders.

TANGO 364

20 cDNA clones (designated jthke076a05 and jthkf069g11) encoding at least a portion of human TANGO 364 protein were isolated from a human fetal skin cDNA library by computerized sequence analysis of library ORFs which encode a signal sequence (SPOT analysis). Human TANGO 364 protein is predicted by structural analysis to be a transmembrane protein.

25 The full length of the cDNA encoding human TANGO 364 protein (Figure 3; SEQ ID NO: 31) is 3510 nucleotide residues. The ORF of this cDNA, nucleotide residues 235 to 1764 of SEQ ID NO: 31 (i.e., SEQ ID NO: 32), encodes a 510-amino acid residue protein (Figure 3; SEQ ID NO: 33), corresponding to a 479-residue transmembrane protein. TANGO 364 cDNA can exist in an alternatively-spliced form,

as listed in Figures 3G through 3I. In this alternative form, TANGO 364 cDNA is 2510 nucleotide residues in length (SEQ ID NO: 41). The ORF of this cDNA, nucleotide residues 2 to 898 of SEQ ID NO: 41 (i.e., SEQ ID NO: 42), encodes a 299-amino acid residue protein (Figure 3; SEQ ID NO: 43) which has the same sequence as the portions of full length TANGO 364 protein indicated in the alignment (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4) listed in Figures 3J and 3K. In the discussion which follows, the full length and alternatively-spliced forms of TANGO 364 molecules are referred to individually and collectively as TANGO 364 molecules of the corresponding type (e.g., cDNA and protein).

The invention thus includes purified human TANGO 364 protein, both in the form of the immature 510 amino acid residue protein (SEQ ID NO: 33) and in the form of the mature 479 amino acid residue protein (SEQ ID NO: 35). Mature human TANGO 364 proteins can be synthesized without the signal sequence polypeptide at the amino terminus thereof, or it can be synthesized by generating immature TANGO 364 protein and cleaving the signal sequence therefrom.

The invention also includes nucleic acid molecules which encode a polypeptide of the invention. Such nucleic acids include, for example, a DNA molecule having the nucleotide sequence listed in SEQ ID NO: 31 or some portion thereof, such as the portion which encodes mature human TANGO 364 protein, immature human TANGO 364 protein, or a domain of human TANGO 364 protein. These nucleic acids are collectively referred to as nucleic acids of the invention.

TANGO 364 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features.

A common domain present in TANGO 364 proteins is a signal sequence. In one embodiment, a TANGO 364 protein contains a signal sequence corresponding to the portion of the protein from amino acid residue 1 to about amino acid residue 31 of SEQ ID NO: 33 (SEQ ID NO: 34). It is recognized that the carboxyl terminal boundary of the signal sequence can be located one or two residues from the residue

identified above (i.e., at residue 29, 30, 31, 32, or 33 of SEQ ID NO: 33). The signal sequence is cleaved during processing of the mature protein.

TANGO 364 proteins can include an extracellular domain. The human TANGO 364 protein extracellular domain is located from about amino acid residue 32 to amino acid residue 345 of SEQ ID NO: 33 (i.e., the extracellular domain has the sequence SEQ ID NO: 36).

In addition, TANGO 364 can include a transmembrane domain. In one embodiment, a TANGO 364 protein of the invention contains a transmembrane domain corresponding to about amino acid residues 346 to 370 of SEQ ID NO:33 (i.e., the transmembrane domain has the sequence SEQ ID NO: 37).

The present invention includes TANGO 364 proteins having a cytoplasmic domain, particularly including proteins having a carboxyl-terminal cytoplasmic domain. As used herein, a "cytoplasmic domain" refers to a portion of a protein which is localized to the cytoplasmic side of a lipid bilayer of a cell when a nucleic acid encoding the protein is expressed in the cell. The human TANGO 364 cytoplasmic domain is located from about amino acid residue 371 to amino acid residue 510 of SEQ ID NO: 33 (i.e., the cytoplasmic domain has the sequence SEQ ID NO: 38).

In an alternative embodiment, TANGO 364 proteins have a cytoplasmic domain located from about amino acid residue 32 to amino acid residue 345 of SEQ ID NO: 33 (i.e., the extracellular domain has the sequence SEQ ID NO: 36); a transmembrane domain corresponding to about amino acid residues 346 to 370 of SEQ ID NO: 33 (i.e., the transmembrane domain has the sequence SEQ ID NO: 37); and an extracellular domain located from about amino acid residue 371 to amino acid residue 510 of SEQ ID NO: 33 (i.e., the extracellular domain has the sequence SEQ ID NO: 38).

TANGO 364 proteins typically comprise a variety of potential post-translational modification sites (often within an extracellular domain), such as those described herein in Table VI, as predicted by computerized sequence analysis of

TANGO 364 proteins using amino acid sequence comparison software (comparing the amino acid sequence of TANGO 364 with the information in the PROSITE database {rel. 12.2; Feb, 1995} and the Hidden Markov Models database {Rel. PFAM 3.3}).

Table VI

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 33	Amino Acid Sequence
N-glycosylation site	281 to 284	NWTR
	430 to 433	NSSC
	489 to 492	NGTL
Protein kinase C phosphorylation site	26 to 28	TGR
	192 to 194	SSR
	195 to 197	SFK
	249 to 251	SVR
	322 to 324	SSR
	339 to 341	SGK
	383 to 385	TQK
	397 to 399	SIR
	426 to 428	SLK
	450 to 452	TVR
	465 to 467	SGR
	491 to 493	TLR
Casein kinase II phosphorylation site	283 to 286	TRLD
	322 to 325	SSRD
	410 to 413	SQPE
	426 to 429	SLKD
	450 to 453	TVRE
	456 to 459	TQTE

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Table VI

N-myristoylation site	135 to 140	GSFQAR
	162 to 167	GQGLTL
	189 to 194	GTTSSR
	218 to 223	GQPLTC
	311 to 316	GIYVCH
	354 to 359	GVIAAL
	464 to 469	GSGRAE
	477 to 482	GIKQAM
	490 to 495	GTLRAK
	500 to 505	GIYING
Cell attachment sequence	55 to 57	RGD
Immunoglobulin-/major histocompatibility protein-like (Ig-/MHC-like) domain	45 to 129	See Fig. 3
	162 to 225	
	263 to 317	

In various embodiments, the protein of the invention has at least 1, 2, 4, 6, 10,
15, or 20 or more of the post-translational modification sites described herein in Table
VI.

Examples of additional domains present in human TANGO 364 protein include
the RGD cell attachment sequence and Ig-/MHC-like domains. In one embodiment,
the protein of the invention has at least one domain that is at least 55%, preferably at
least about 65%, more preferably at least about 75%, yet more preferably at least about
85%, and most preferably at least about 95% identical to one of the Ig-/MHC-like
domains described herein in Table VI. Preferably, the protein of the invention has at
least one Ig-/MHC-like domain and one RGD cell attachment sequence.

Ig-/MHC-like domains are conserved among immunoglobulin (Ig) constant
(CL) regions and one of the three extracellular domains of major histocompatibility

proteins (MHC). Ig-/MHC-like domains are involved in protein-to-protein and protein-to-ligand binding.

The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that human TANGO 364 protein includes an
5 approximately 31 amino acid signal peptide (amino acid residues 1 to about 31 of SEQ ID NO: 33; SEQ ID NO: 34) preceding the mature TANGO 364 protein (amino acid residues 32 to 510 of SEQ ID NO: 33; SEQ ID NO: 35). Human TANGO 364 protein includes an extracellular domain (amino acid residues 32 to 345 of SEQ ID NO: 33; SEQ ID NO: 36), a transmembrane domain (amino acid residues 346 to 370 of SEQ ID
10 NO: 33; SEQ ID NO: 37), and a cytoplasmic domain (amino acid residues 371 to 510 of SEQ ID NO: 33; SEQ ID NO: 38).

Figure 3F depicts a hydrophobicity plot of human TANGO 364 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region
15 which corresponds to amino acid residues 1 to about 31 of SEQ ID NO: 33 is the signal sequence of human TANGO 364 (SEQ ID NO: 34), and the hydrophobic region which corresponds to amino acid residues 346 to 370 of SEQ ID NO: 33 is the transmembrane region of TANGO 364 (SEQ ID NO: 37). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a
20 protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 364 protein from about amino acid residue 371 to about amino acid residue 410 appears to be located at or near the surface of the protein, while the region from about amino acid residue 235 to about amino acid residue 245 appears not to be located at or near the surface.

25 The predicted molecular weight of human TANGO 364 protein without modification and prior to cleavage of the signal sequence is about 55.5 kilodaltons. The predicted molecular weight of the mature human TANGO 364 protein without modification and after cleavage of the signal sequence is about 52.1 kilodaltons.

TANGO 364 exhibits limited sequence similarity to numerous cell surface proteins, including proteins which serve as cell surface antigens, proteoglycans, and virus receptors.

5 Uses of TANGO 364 Nucleic acids,
 Polypeptides, and Modulators Thereof

 TANGO 364 proteins are involved in disorders which affect both tissues in which they are normally expressed and tissues in which they are normally not expressed. Based on the observations that cDNA corresponding to TANGO 364
10 occurs in a human fetal skin cDNA library, it is evident that TANGO 364 protein is involved in one or more biological processes which occur in skin tissues. In particular, TANGO 364 is involved in modulating one or more of growth, proliferation, survival, differentiation, activity, morphology, and movement/migration of skin cells. Thus, TANGO 364 has a role in disorders which affect skin cells and one or more of their
15 growth, proliferation, survival, differentiation, activity, morphology, and movement/migration, as well as the biological function of skin.

 There are several indications that TANGO 364 is a cell surface protein which is involved in binding a ligand to the cell which expresses the protein. For instance, presence in TANGO 364 of an amino terminal extracellular domain that includes three
20 Ig-/MHC-like domains exemplifies the cell-surface ligand-binding capability of TANGO 364. In addition, the amino acid sequence similarity which TANGO 364 exhibits with respect to several other cell surface ligand-binding proteins reinforces this view. Presence in TANGO 364 of an Ig-/MHC-like domain indicates that the corresponding region of TANGO 364 is structurally similar to this conserved
25 extracellular region, and that TANGO 364 is involved in binding one or more of a ligand and a protein (including, for example, a serum protein and a cell-surface protein of another cell). Thus, molecules (e.g., antibodies and short peptides) which are able to interact specifically with an Ig-/MHC-like domain of a TANGO 364 protein can inhibit

binding of TANGO 364 with its normal ligand, thereby disrupting one or more physiological processes associated with such binding. Furthermore, polypeptides (including, for example, full-length TANGO 364 protein and polypeptides of at least about 25 to 50 amino acid residues) which comprise all or part of an Ig-/MHC-like domain of TANGO 364 can bind with one or more of the normal ligands of TANGO 364, thereby replicating the normal physiological effect of binding between TANGO 364 and the ligand or inhibiting binding of endogenous TANGO 364 with the ligand. Therefore, TANGO 364 protein, polypeptides having at least one Ig-/MHC-like domain thereof, and molecules capable of interacting with such a domain are useful for prognosticating, diagnosing, treating, and inhibiting disorders associated with aberrant binding of TANGO 364 and its normal ligand.

TANGO 364 is involved in binding an animal cell which expresses it with one or more of a protein (e.g., an antibody, an major histocompatibility protein, a lectin, or another cell surface protein), a small molecule (e.g., a sugar, a hormone, or another molecule having a molecular weight less than about 5000, 1000, or 500 or less Daltons), a component of the extracellular matrix (e.g., a collagen protein), another cell of the same animal, a bacterial or fungal cell, and a virus. Thus, TANGO 364 is involved in modulating cell-to-cell adhesion, tissue and extracellular matrix invasivity of cells, infectivity of cells by pathogens (e.g., bacteria and viruses), endocrine signaling processes, tissue developmental and organizational processes, and the like. Thus, TANGO 364 is involved in disorders in which these physiological processes are relevant.

Disorders associated with aberrant cell-to-cell adhesion include tumor growth and metastasis, malformation or degradation of neurological connections, autoimmune disorders, immune insufficiency disorders, atherosclerosis, arteriosclerosis, abnormal blood coagulation, and the like. Disorders associated with tissue and extracellular matrix invasivity of cells include tumor metastasis, osteoporosis, inflammation, and the like. Disorders associated with pathogenic infections include infections associated

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with bacteria, fungi, mycoplasmas, viruses, eukaryotic parasites, and the like. Disorders associated with aberrant endocrine signaling processes include, for example, diabetes mellitus, hypoglycemia, glucagon disorders, pituitary disorders (e.g., diabetes insipidus), thyroid disorders (e.g., hyper- and hypothyroidism), adrenal disorders (e.g., Addison's disease, adrenal virilism, Cushing's syndrome, and hyperaldosteronism), multiple endocrine neoplasias, and polyglandular deficiency syndromes. Disorders associated with aberrant tissue developmental and organizational processes include, for example, birth defects, benign and malignant carcinogenesis, neurodegenerative disorders (e.g., Alzheimer's disease), and the like. TANGO 364 proteins, nucleic acids encoding them, and agents (e.g., antibodies, peptides, and small molecules) that modulate activity or expression of either of these can be used to prognosticate, diagnose, treat, and inhibit one or more of these disorders.

TANGO 405

15 A cDNA clone (designated jthLa152h06) encoding at least a portion of human TANGO 405 protein was isolated from a human mixed lymphocyte reaction cDNA library. A corresponding murine cDNA (designated jtmMa025a11) was isolated from a long-term bone marrow cDNA library. Human and murine TANGO 405 proteins are secreted proteins.

20 The full length of the cDNA encoding human TANGO 405 protein (Figure 4; SEQ ID NO: 51) is 3114 nucleotide residues in length. The open reading frame (ORF) of this cDNA, nucleotide residues 154 to 780 of SEQ ID NO: 51 (i.e., SEQ ID NO: 52), encodes a 209-amino acid residue protein (Figure 4; SEQ ID NO: 53), corresponding to a 161-residue secreted protein.

25 The invention thus includes purified human TANGO 405 protein, both in the form of the immature 209 amino acid residue protein (SEQ ID NO: 53) and in the form of the mature 161 amino acid residue protein (SEQ ID NO: 55). The invention also includes purified murine TANGO 405 protein, both in the form of the immature 178-

amino acid residue protein (SEQ ID NO: 63) and in the form of the mature, secreted
136-amino acid residue protein (SEQ ID NO: 65). Mature human or murine TANGO
405 protein can be synthesized without the signal sequence polypeptide at the amino
terminus thereof, or they can be synthesized by generating immature TANGO 405
5 protein and cleaving the signal sequence therefrom.

The invention also includes nucleic acid molecules which encode a polypeptide
of the invention. Such nucleic acids include, for example, a DNA molecule having the
nucleotide sequence listed in SEQ ID NO: 51 or some portion thereof or SEQ ID NO:
61 or some portion thereof, such as the portion which encodes mature human or murine
10 TANGO 405 protein, immature human or murine TANGO 405 protein, or a domain of
human or murine TANGO 405 protein. These nucleic acids are collectively referred to
as nucleic acids of the invention.

TANGO 405 proteins and nucleic acid molecules encoding them comprise a
family of molecules having certain conserved structural and functional features.

A common domain present in TANGO 405 proteins is a signal sequence. In
one embodiment, a TANGO 405 protein contains a signal sequence corresponding to
the portion of the protein from amino acid residue 1 to about amino acid residue 48 of
SEQ ID NO: 53 (SEQ ID NO: 54) or to the portion of the protein from amino acid
residue 1 to about amino acid residue 42 of SEQ ID NO: 63 (SEQ ID NO: 64). It is
15 recognized that the carboxyl terminal boundary of the signal sequence can be located
one or two residues from the residue identified above (i.e., at residue 46, 47, 48, 49, or
50 of SEQ ID NO: 53 or at residue 40, 41, 42, 43 or 44 of SEQ ID NO: 63). The signal
sequence is cleaved during processing of the mature protein.

TANGO 405 proteins typically comprise a variety of potential post-
25 translational modification sites (often within an extracellular domain), such as those
described herein in Table VII (for human TANGO 405) and VIII (for murine TANGO
405), as predicted by computerized sequence analysis of TANGO 405 proteins using
amino acid sequence comparison software (comparing the amino acid sequence of

TANGO 405 with the information in the PROSITE database {rel. 12.2; Feb, 1995} and the Hidden Markov Models database {Rel. PFAM 3.3}).

Table VII

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 53	Amino Acid Sequence
N-glycosylation site	131 to 134	NESF
	170 to 173	NHSA
cAMP- or cGMP-dependent protein kinase phosphorylation site	52 to 55	KRLS
	197 to 200	RRNS
Protein kinase C phosphorylation site	10 to 12	TEK
	17 to 19	SLR
	50 to 52	TGK
	82 to 84	SWK
	196 to 198	TRR
Casein kinase II phosphorylation site	46 to 49	TYGE
	94 to 97	SSEE
	101 to 104	SKSE
	119 to 122	TEAE
	155 to 158	TPYE
	200 to 203	SICE
Tyrosine kinase phosphorylation site	52 to 60	KRLSELHSY
N-myristoylation site	25 to 30	GISIAL
	77 to 82	GCCPAS
Amidation site	50 to 53	TGKR
C-type lectin domain signature	176 to 202	See Fig. 4
C-type lectin domain	105 to 202	See Fig. 4

Table VIII

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 63	Amino Acid Sequence
N-glycosylation site	136 to 139	NESL
	155 to 158	NGSM
Protein kinase C phosphorylation site	20 to 22	TLR
	54 to 56	SRR
	77 to 79	SEK
	99 to 101	STK
	162 to 164	SVK
Casein kinase II phosphorylation site	99 to 102	STKE
	106 to 109	STSE
	124 to 127	TEAE
Tyrosine kinase phosphorylation site	55 to 63	RRLYELHTY
N-myristoylation site	16 to 21	GVCWTL
	73 to 78	GTMVSE
	82 to 87	GCCPNH
C-type lectin domain	110 to 180	See Fig. 4

In various embodiments, the protein of the invention has at least 1, 2, 4, 6, 10, 15, or 20 or more of the post-translational modification sites described herein in Tables VII and VIII.

- 5 Examples of additional domains present in human and murine TANGO 405 protein include a C-type lectin domain and a corresponding signature sequence. In one embodiment, the protein of the invention has a C-type lectin domain or signature sequence that is at least 55%, preferably at least about 65%, more preferably at least about 75%, yet more preferably at least about 85%, and most preferably at least about
- 10 95% identical to one of those described herein in Tables VII and VIII.

5 C-type lectin domains are conserved among proteins (e.g., animal lectins) which are involved in calcium-dependent binding of carbohydrates, although it has recently been recognized that these domains can also be involved in binding of proteins (Drickamer, 1988, J. Biol. Chem. 263:9557-9560; Drickamer, 1993, Prog. Nucl. Acid Res. Mol. Biol. 45:207-232; Drickamer, 1993, Curr. Opin. Struct. Biol. 3:393-400). C-type lectins and their relevant properties are described in greater in P.C.T. Publication No. WO 98/28332, which, as with all references cited herein, is incorporated by reference.

10 In PCT Publication No. WO 98/28332, a cDNA encoding murine protein, designated dectin-2, was isolated from dendritic cells and described. Human and murine TANGO 405 proteins exhibit amino acid sequence homology with murine dectin-2. As indicated in the alignment in Figure 4M (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), human TANGO 405 exhibits about 89.0% sequence identity with murine dectin-2. As indicated in the alignment in Figure 4L (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), murine TANGO 405 exhibits about 70.3% sequence identity with murine dectin-2.

20 Another embodiment of a murine TANGO 405 cDNA is shown in Figures 4N to 4P (the cDNA having the sequence SEQ ID NO: 71 and the ORF having the nucleotide sequence SEQ ID NO: 72). In this embodiment murine TANGO 405 includes a translational frame shift, and the amino acid sequence (SEQ ID NO: 73) of murine TANGO 405 is identical to the amino acid sequence reported for murine dectin-2. These data further confirm that human TANGO 405 is the human ortholog of murine dectin-2.

25 The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that human TANGO 405 protein includes an approximately 48 amino acid signal peptide (amino acid residues 1 to about 48 of SEQ ID NO: 53; SEQ ID NO: 54) preceding the mature TANGO 405 protein (amino acid

residues 49 to 209 of SEQ ID NO: 53; SEQ ID NO: 55). It is recognized that both human and murine TANGO 405 can, at least transiently, exist in an integral membrane form, at least until cleavage of the corresponding signal sequence (i.e., either during or following translation of the complete TANGO 405 protein).

5 Figure 4D depicts a hydrophobicity plot of human TANGO 405 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 48 of SEQ ID NO: 53 is the signal sequence of human TANGO 405 (SEQ ID NO: 54). As described elsewhere herein, 10 relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 405 protein from about amino acid residue 90 to about amino acid residue 105 appears to be located at or near the surface of the protein, while the region from about amino acid residue 110 to 15 about amino acid residue 120 appears not to be located at or near the surface.

The predicted molecular weight of human TANGO 405 protein without modification and prior to cleavage of the signal sequence is about 24.0 kilodaltons. The predicted molecular weight of the mature human TANGO 405 protein without modification and after cleavage of the signal sequence is about 18.6 kilodaltons.

20 The full length of the cDNA encoding murine TANGO 405 protein (Figure 4; SEQ ID NO: 61) is 821 nucleotide residues, although this cDNA sequence is incomplete. The ORF of this cDNA, nucleotide residues 174 to 707 of SEQ ID NO: 61 (i.e., SEQ ID NO: 62), encodes a protein comprising at least 178 amino acid residues (Figure 4; SEQ ID NO: 63).

25 The signal peptide prediction program SIGNALP (Nielsen et al. (1997) Protein Engineering 10:1-6) predicted that murine TANGO 405 protein includes an approximately 42 amino acid signal peptide (amino acid residues 1 to about 42 of SEQ ID NO: 63; SEQ ID NO: 64) preceding the mature TANGO 405 protein (amino acid

residues 43 to 178 of SEQ ID NO: 63; SEQ ID NO: 65). Murine TANGO 405 protein is a secreted protein.

Figure 4G depicts a hydrophobicity plot of murine TANGO 405 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 42 of SEQ ID NO: 63 is the signal sequence of murine TANGO 405 (SEQ ID NO: 64). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 405 protein from about amino acid residue 95 to about amino acid residue 110 appears to be located at or near the surface of the protein, while the region from about amino acid residue 110 to about amino acid residue 120 appears not to be located at or near the surface

The predicted molecular weight of murine TANGO 405 protein without modification and prior to cleavage of the signal sequence is about 20.0 kilodaltons. The predicted molecular weight of the mature murine TANGO 405 protein without modification and after cleavage of the signal sequence is about 25.3 kilodaltons.

Human and murine TANGO 405 proteins exhibit considerable sequence similarity, as indicated herein in Figure 4H. Figure 4H depicts an alignment of human and murine TANGO 405 amino acid sequences (SEQ ID NOs: 53 and 63, respectively). In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap penalties -12/-4), the proteins are 51.7% identical in the overlapping region (i.e., amino acid residues 1-209 of SEQ ID NO: 53 and amino acid residues 1-178 of SEQ ID NO: 63). The human and murine ORFs encoding TANGO 405 are 74.5% identical in the 541 nucleotide residue overlapping region, as assessed using the same software and parameters and as indicated in Figures 4I through 4K. The nucleotide sequences encoding human and murine TANGO 405 (i.e., SEQ ID NOs: 51 and 61) are about 71.2% identical in the

838 nucleotide residue overlapping region, as assessed using the LALIGN software (Myers and Miller (1989) CABIOS, ver. 2.0; pam120.mat scoring matrix; gap penalties -12/-4).

5 Uses of TANGO 405 Nucleic acids,
 Polypeptides, and Modulators Thereof

 TANGO 405 proteins are involved in disorders which affect both tissues in which they are normally expressed and tissues in which they are normally not expressed. Based on the observations that cDNA corresponding to TANGO 405
10 occurs in a human mixed lymphocyte reaction cDNA library and in a murine long-term bone marrow cDNA library, it is evident that TANGO 405 protein is involved in one or more biological processes which occur in these tissues (i.e., in blood-related tissues, such as tissues containing lymphocytes). In particular, TANGO 405 is involved in modulating one or more of growth, proliferation, survival, differentiation, activity,
15 morphology, and movement/migration of cells of these tissues. TANGO 405 is involved in modulating the structure of extracellular matrix which contacts or is in fluid communication with cells of these tissues. Thus, TANGO 405 has a role in disorders which affect these cells and one or more of their growth, proliferation, survival, differentiation, activity, morphology, and movement/migration, as well as the
20 biological function of tissues comprising one or more of these types of cells.

 Presence of a C-type lectin domain in TANGO 405 is an indication that this protein is capable of specifically recognizing particular surfaces, such as the surface of cells of a particular type. Further supportive of this observation is the fact that human TANGO 405 protein exhibits significant sequence homology with murine dectin-2
25 protein. Murine dectin-2 has been shown to be expressed by murine dendritic cells, and has also been shown to be involved in activation of naive T cells. Murine dectin-2 can also be involved in inflammatory and non-T cell-mediated immune responses. Thus, human and murine TANGO 405 are also involved in activating or inhibiting one

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or more types of lymphocytes, thereby modulating T cell-mediated immune responses, non-T cell-mediated immune responses, inflammatory responses, and other components of the immune response in mammals. It is recognized that the amino acid sequence differences among murine dectin-2, human TANGO 405, and murine

5 TANGO 405 can lead to different lymphocyte-activating capacities for these three proteins. Human and murine TANGO 405 proteins are involved both in normal activation of lymphocytes (e.g., in response to the presence of a pathogen in a tissue) and in aberrant activation of lymphocytes (e.g., as in auto-immune and immune inflammatory disorders (e.g., asthma), in disorders characterized by an insufficient

10 immune response, and in disorders characterized by non-controlled proliferation of lymphocytes). TANGO 405 proteins are thus involved in a variety of disorders relating to aberrant lymphocyte activation or proliferation. Examples of disorders include leukemias (e.g., ALL, CML, CLL, and myelodysplastic syndrome), lymphomas (e.g., Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma,

15 and mycosis fungoides), plasma cell dyscrasias, auto-immune disorders such as multiple sclerosis, bacterial and viral infections (e.g., acquired immune deficiency syndrome), leukopenias, eosinophilic disorders such as idiopathic hypereosinophilic syndrome, and the like. TANGO 405 proteins, nucleic acids encoding them, and agents that modulate activity or expression of either of these can be used to

20 prognosticate, diagnose, treat, and inhibit one or more of these disorders.

M019 (also designated TANGO 533)

A cDNA encoding at least a portion of human M019 protein was isolated from a human adipose tissue cDNA library. The human M019 protein is predicted by

25 structural analysis to be a secreted protein.

The full length of the cDNA encoding human M019 protein (Figure 5; SEQ ID NO: 81) is 1202 nucleotide residues. The ORF of this cDNA, nucleotide residues 331

to 585 of SEQ ID NO: 81 (Figure 5; SEQ ID NO: 82), encodes a 85-amino acid secreted protein (Figure 5; SEQ ID NO: 83).

5 The invention thus includes purified human M019 protein, both in the form of the immature 85 amino acid residue protein (SEQ ID NO: 83) and in the form of the mature 62 amino acid residue protein (SEQ ID NO: 85). Mature human M019 protein can be synthesized without the signal sequence polypeptide at the amino terminus thereof, or it can be synthesized by generating immature M019 protein and cleaving the signal sequence therefrom.

10 The invention also includes nucleic acid molecules which encode a polypeptide of the invention. Such nucleic acids include, for example, a DNA molecule having the nucleotide sequence listed in SEQ ID NO: 81 or some portion thereof, such as the portion which encodes mature M019 protein, immature M019 protein, or a domain of M019 protein. These nucleic acids are collectively referred to as nucleic acids of the invention.

15 M019 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features. Each of these molecules is included in the invention. As used herein, the term "family" is intended to mean two or more proteins or nucleic acid molecules having a common or similar domain structure and having sufficient amino acid or nucleotide sequence identity as defined herein. Family members can be from either the same or different species. For
20 example, a family can comprise two or more proteins of human origin, or can comprise one or more proteins of human origin and one or more of non-human origin.

A common domain present in M019 proteins is a signal sequence. In one embodiment, a M019 protein contains a signal sequence corresponding to amino acid
25 residues 1 to 23 of SEQ ID NO: 83 (SEQ ID NO: 84). The signal sequence is cleaved during processing of the mature protein.

M019 proteins are secreted proteins, and thus include an 'extracellular domain,' both in the mature protein (i.e., wherein the entire mature protein is an 'extracellular

domain') and in the immature protein (e.g., wherein the signal sequence, residues 1-23 of SEQ ID NO: 83, is embedded in the membrane prior to cleavage, and the remainder of the protein, about residues 24-85 is extracellular). As used herein, an "extracellular domain" refers to a portion of a protein which is localized to the non-cytoplasmic side of a lipid bilayer of a cell when a nucleic acid encoding the protein is expressed in the cell.

M019 proteins typically comprise a variety of potential post-translational modification sites (often within an extracellular domain), such as those described herein in Table IX, as predicted by computerized sequence analysis of M019 proteins using amino acid sequence comparison software (comparing the amino acid sequence of M019 with the information in the PROSITE database {rel. 12.2; Feb, 1995} and the Hidden Markov Models database {Rel. PFAM 3.3}). In certain embodiments, a protein of the invention has at least 1, 2, 3, or all 4 of the post-translational modification sites listed in Table IX.

Table IX

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 83	Amino Acid Sequence
Protein kinase C phosphorylation site	47 to 49	SNR
	75 to 77	TMK
Casein kinase II phosphorylation site	47 to 50	SNRE
N-myristoylation site	34 to 49	GQDSNL

M019 exhibits no significant amino acid sequence similarity with any known protein. Thus, M019 appears to be a novel protein.

Figure 5C depicts a hydrophobicity plot of human M019 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 23 of SEQ ID NO: 83 is the signal sequence of human M019 (SEQ ID NO: 84). As described elsewhere herein, relatively hydrophilic

regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human M019 protein from about amino acid residue 63 to about amino acid residue 80 appears to be located at or near the surface of the protein, while the region from about amino acid residue 55 to about amino acid residue 60 appears not to be located at or near the surface.

Uses of M019 Nucleic acids,
Polypeptides, and Modulators Thereof

M019 proteins are involved in disorders which affect both tissues in which they are normally expressed and tissues in which they are normally not expressed. Based on the observation that M019 is expressed in adipose tissue, M019 protein is involved in one or more biological processes which occur in these tissues and in disorders which affect adipose tissue. Such disorder include, for example, obesity, hypercholesterolemia, hyperlipidemia, hyperlipoproteinemia, diabetes, stroke, liver fibrosis, atherosclerosis, arteriosclerosis, and coronary artery disease.

By virtue of its size and the presence of a pair of cysteine residues in its mature form, M019 resembles chemokine molecules, and it therefore believed to be involved in modulating adipose tissue processes involving interaction of cells (e.g., leukocytes) and proteins (e.g., lipoproteins) with the surface of adipose tissue cells. Such processes include, for example, uptake, release, metabolism, and storage of lipids (e.g., triglycerides), cholesterol, lipoproteins, and the like.

M019 exhibits limited sequence similarity with pancreatic proteins, indicating that this protein is involved in physiological processes of the pancreas and in pancreatic disorders, as well as other disorders. Pancreatic disorders in which M019 can be involved include those pancreatic disorders described elsewhere in this disclosure.

Tables A and B summarize sequence data corresponding to the nucleic acids and proteins disclosed herein.

Table A

Protein Designation	SEQ ID NOs			Depicted in	ATCC®
	cDNA	ORF	Protein	Figure #	Accession #
human TANGO 273	1	2	3	1	207185
murine TANGO 273	11	12	13	1	207221
human TANGO 325	21	22	23	2	PTA-147
human TANGO 364	31	32	33	3	PTA-425
human TANGO 364 (alternative form)	41	42	43	3	PTA-425
human TANGO 405	51	52	53	4	PTA-424
murine TANGO 405	61	62	63	4	---
murine TANGO 405 (alternative form)	71	72	73	4	---
human M019	81	82	83	5	---

Table B

Protein Desig.	Signal Sequence ¹	Mature Protein	Extracellular Domain(s) ²	Transmembrane Domain(s)	Cytoplasmic Domain(s) ²
		SEQ ID NOs			
hum. TANGO 273	1 to 22	23 to 172	23 to 60	61 to 81	82 to 172
mur. TANGO 273	1 to 22	23 to 172	23 to 60	61 to 81	82 to 172
hum. TANGO 325	1 to 31	32 to 622	32 to 529	530 to 547	548 to 622
hum. TANGO 364	1 to 31	32 to 510	32 to 345	346 to 370	371 to 510
hum. TANGO 405	1 to 48	49 to 209	49 to 209	N/A	N/A
mur. TANGO 405	1 to 52	53 to 178	53 to 178	N/A	N/A
hum. M019	1 to 23	24 to 82	24 to 82		
Amino Acid Residues					

Notes for Table B:

¹ It is recognized that the carboxyl terminal boundary of the signal sequence can be ± 1 or 2 residues from that indicated.² It is recognized that 'extracellular' and cytoplasmic' domains can have the opposite orientation in certain embodiments, as described herein.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

5 One aspect of the invention pertains to isolated nucleic acid molecules that encode a polypeptide of the invention or a biologically active portion thereof, as well as nucleic acid molecules sufficient for use as hybridization probes to identify nucleic acid molecules encoding a polypeptide of the invention and fragments of such nucleic acid molecules suitable for use as PCR primers for the amplification or
10 mutation of nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded.

15 An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of
20 the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5, 4, 3, 2, 1, 0.5, or 0.1 kilobases of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be
25 substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule having the nucleotide sequence of all or a portion of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a complement thereof, or which has a nucleotide sequence comprising one of these sequences, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequences of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___ as a hybridization probe, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook et al., Eds., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or a portion thereof. A nucleic acid molecule which is complementary to a given nucleotide

sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize with the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise a portion of a nucleic acid sequence encoding a full length polypeptide of the invention, such as a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a polypeptide of the invention. The nucleotide sequence determined from cloning one gene allows generation of probes and primers designed for identifying and/or cloning homologs in other cell types, e.g., from other tissues, as well as homologs from other mammals. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions with at least about 15, preferably about 25, more preferably about 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1410, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, or 3500 or more consecutive nucleotides of the sense or anti-sense sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, or of a naturally occurring mutant of any of these sequences.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences encoding the same protein molecule encoded by a selected nucleic acid molecule. The probe comprises a label group attached thereto, e.g., a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which aberrantly express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells

from a subject, e.g., detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

A nucleic acid fragment encoding a biologically active portion of a polypeptide of the invention can be prepared by isolating a portion of one of SEQ ID
5 NOs: 2, 12, 22, 32, 42, 52, 62, 72, and 82 expressing the encoded portion of the polypeptide protein (e.g., by recombinant expression in vitro), and assessing the activity of the encoded portion of the polypeptide.

The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42,
10 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, due to degeneracy of the genetic code and thus encode the same protein as that encoded by the nucleotide sequence of one of SEQ ID NOs: 2, 12, 22, 32, 42, 52, 62, 72, and 82.

In addition to the nucleotide sequences of one of SEQ ID NOs: 2, 12, 22, 32,
15 42, 52, 62, 72, and 82, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (e.g., the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An
20 allele is one of a group of genes which occur alternatively at a given genetic locus.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid
25 residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two

sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = # of identical positions / total # of positions {e.g., overlapping positions} × 100). In one embodiment, the two sequences are the same length.

5 The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. 10 (1990) J. Mol. Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped 15 alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be 20 used. See <http://www.ncbi.nlm.nih.gov>.

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the local homology algorithm of Smith and Waterman (Advances in Applied Mathematics 2: 482-489 (1981)). Such an algorithm is incorporated into the BestFit program, which is part of the Wisconsin™ package, and 25 is used to find the best segment of similarity between two sequences. BestFit reads a scoring matrix that contains values for every possible GCG symbol match. The program uses these values to construct a path matrix that represents the entire surface of comparison with a score at every position for the best possible alignment to that

point. The quality score for the best alignment to any point is equal to the sum of the scoring matrix values of the matches in that alignment, less the gap creation penalty multiplied by the number of gaps in that alignment, less the gap extension penalty multiplied by the total length of all gaps in that alignment. The gap creation and gap extension penalties are set by the user. If the best path to any point has a negative value, a zero is put in that position.

After the path matrix is complete, the highest value on the surface of comparison represents the end of the best region of similarity between the sequences. The best path from this highest value backwards to the point where the values revert to zero is the alignment shown by BestFit. This alignment is the best segment of similarity between the two sequences. Further documentation can be found at <http://ir.ucdavis.edu/GCGhelp/bestfit.html#algorithm>.

Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti (1994) *Comput. Appl. Biosci.*, 10:3-5; and FASTA described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci.* 85:2444-8. Within FASTA, ktup is a control option that sets the sensitivity and speed of the search. If ktup=2, similar regions in the two sequences being compared are found by looking at pairs of aligned residues; if ktup=1, single aligned amino acids are examined. ktup can be set to 2 or 1 for protein sequences, or from 1 to 6 for DNA sequences. The default if ktup is not specified is 2 for proteins and 6 for DNA. For a further description of FASTA parameters, see <http://bioweb.pasteur.fr/docs/man/man/fasta.1.html#sect2>, the contents of which are incorporated herein by reference.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide

sequence. For example, the TANGO 273 gene exhibits significant homology with a portion of chromosome 7 between chromosomal markers D7S2467 and D7S2552. Allelic variants of any of this gene can be identified by sequencing the corresponding chromosomal portion at the indicated location in multiple individuals.

5 As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be
10 readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

15 Moreover, nucleic acid molecules encoding proteins of the invention from other species (homologs), which have a nucleotide sequence which differs from that of the human proteins described herein are within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologs of a cDNA of the invention can be isolated based on their identity to human nucleic acid
20 molecules using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. For example, a cDNA encoding a soluble form of a membrane-bound protein of the invention can be isolated based on its hybridization with a nucleic acid molecule encoding all or part of the membrane-bound form. Likewise, a cDNA
25 encoding a membrane-bound form can be isolated based on its hybridization with a nucleic acid molecule encoding all or part of the soluble form.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 (25, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 500,

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600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800,
3000, or 3500 or more) nucleotides in length and hybridizes under stringent
conditions to the nucleic acid molecule comprising the nucleotide sequence,
preferably the coding sequence, of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32,
5 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the
clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-
425, PTA-424, ____, and ____, or a complement thereof. As used herein, the term
"hybridizes under stringent conditions" is intended to describe conditions for
hybridization and washing under which nucleotide sequences at least 60% (65%,
10 70%, preferably 75%) identical to each other typically remain hybridized with each
other. Such stringent conditions are known to those skilled in the art and can be
found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989),
6.3.1-6.3.6. A example of stringent hybridization conditions are hybridization in 6×
sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more
15 washes in 0.2× SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid
molecule of the invention that hybridizes under stringent conditions to the sequence
of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81,
82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession
numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ____, and ____, or a
20 complement thereof, corresponds to a naturally-occurring nucleic acid molecule. As
used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA
molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural
protein).

In addition to naturally-occurring allelic variants of a nucleic acid molecule
25 of the invention sequence that can exist in the population, the skilled artisan will
further appreciate that changes can be introduced by mutation thereby leading to
changes in the amino acid sequence of the encoded protein, without altering the
biological activity of the protein. For example, one can make nucleotide

substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino acid residues that are conserved among the homologs of various species (e.g., murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a polypeptide of the invention that contain changes in amino acid residues that are not essential for activity. Such polypeptides differ in amino acid sequence from any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, yet retain biological activity. In one embodiment, the isolated nucleic acid molecule includes a nucleotide sequence encoding a protein that includes an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___.

An isolated nucleic acid molecule encoding a variant protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of any of SEQ ID NOs: 1, 2, 11, 12, 21, 22, 31, 32, 41, 42, 51, 52, 61, 62, 71, 72, 81, 82, and the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___, such that one or more amino acid residue substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated

mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

In one embodiment, a mutant polypeptide that is a variant of a polypeptide of the invention can be assayed for: (1) the ability to form protein:protein interactions with the polypeptide of the invention; (2) the ability to bind a ligand of the polypeptide of the invention; (3) the ability to bind with a modulator or substrate of the polypeptide of the invention; or (4) the ability to modulate a physiological activity of the protein, such as one of those disclosed herein.

The present invention encompasses antisense nucleic acid molecules, i.e., molecules which are complementary to a sense nucleic acid encoding a polypeptide of the invention, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, e.g., all or part of the protein coding region (or open reading frame). An

antisense nucleic acid molecule can be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a polypeptide of the invention. The non-coding regions ("5' and 3' non-translated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

5 An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally
10 occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-
15 fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N₆-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-
20 methylcytosine, 5-methylcytosine, N₆-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N₆-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocyto-
25 sine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-

cloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind with cellular mRNA and/or genomic DNA encoding a selected polypeptide of the invention to thereby inhibit expression, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid
10 molecule which binds with DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration,
15 antisense molecules can be modified such that they specifically bind with receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies which bind with cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the
20 antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an alpha-anomeric nucleic acid molecule. An alpha-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which the strands run parallel
25 to each other (Gaultier et al. (1987) Nucleic Acids Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al. (1987) FEBS Lett. 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach (1988) Nature 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a polypeptide of the invention can be designed based upon the nucleotide sequence of a cDNA disclosed herein. For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the ribozyme active site is complementary to the nucleotide sequence to be cleaved, as described in Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742. Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel and Szostak (1993) Science 261:1411-1418.

The invention includes nucleic acid molecules which form triple helical structures. For example, expression of a polypeptide of the invention can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the polypeptide (e.g., the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) Anticancer Drug Des. 6(6):569-84; Helene (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14(12):807-15. "Expression" of a polypeptide, as used herein, refers individually and collectively to the processes of transcription of DNA to generate an RNA transcript and translation of an RNA to generate the polypeptide.

In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety, or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the

deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow specific hybridization with DNA and RNA under conditions of low ionic strength. Synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols such as those described in Hyrup et al. (1996), *supra*; Perry-O'Keefe et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or anti-gene agents for sequence-specific modulation of gene expression by, e.g., inducing arrest of transcription or translation or by inhibiting replication. PNAs can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup (1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup (1996), *supra*; Perry-O'Keefe et al. (1996) *Proc. Natl. Acad. Sci. USA* 93: 14670-675).

In another embodiment, PNAs can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by formation of PNA-DNA chimeras, or by use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion provides high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and

orientation (Hyrup (1996), supra). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), supra, and Finn et al. (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag et al. (1989) *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser et al. (1975) *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, e.g., Krol et al. (1988) *Bio/Techniques* 6:958-976) or intercalating agents (see, e.g., Zon (1988) *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated with another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated proteins, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to generate antibodies directed against a polypeptide of the invention.

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In one embodiment, the native polypeptide is isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, polypeptides of the invention are produced by recombinant DNA techniques. As an alternative to recombinant expression, a polypeptide of the invention can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals, when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a polypeptide of the invention include polypeptide regions having an amino acid sequence sufficiently identical to or derived from the amino acid sequence of the protein (e.g., the amino acid sequence shown in any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85, or the amino acid sequence encoded by the nucleotide sequence of any of the

clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___), which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein.

Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

Examples of polypeptides are those which have the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___. Other useful proteins are substantially identical (e.g., at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ___, and ___ and retain the functional activity of the protein of the corresponding naturally-occurring protein. Such proteins can differ in amino acid sequence owing, for example, to natural allelic variation or mutagenesis.

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably biologically active) of a polypeptide of the invention operably linked with a heterologous polypeptide (i.e., a polypeptide other than the same polypeptide of the invention). Within the fusion protein, the term "operably linked" is intended to indicate that the polypeptide of the invention and the heterologous polypeptide are fused in-frame

with each other. The heterologous polypeptide can be fused with the amino-terminus or the carboxyl-terminus of the polypeptide of the invention.

One useful fusion protein is a GST fusion protein in which the polypeptide of the invention is fused with the carboxyl terminus of GST sequences. Such fusion proteins can facilitate purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a polypeptide of the invention can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Current Protocols in Molecular Biology, Ausubel et al., eds., John Wiley & Sons, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook et al., supra) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a polypeptide of the invention is fused with sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction in vivo. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a polypeptide of the invention. Inhibition of ligand / receptor interaction can be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (e.g., promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed

against a polypeptide of the invention in a subject, to purify ligands and in screening assays to identify molecules which inhibit the interaction of receptors with ligands. The immunoglobulin fusion protein can, for example, comprise a portion of a polypeptide of the invention fused with the amino-terminus or the carboxyl-terminus of an immunoglobulin constant region, as disclosed in U.S. Patent No. 5,714,147, 5 U.S. Patent No. 5,116,964, U.S. Patent No. 5,514,582, and U.S. Patent No. 5,455,165.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. 10 Alternatively, PCR amplification of gene fragments can be performed using anchor primers which give rise to complementary overhangs between two consecutive gene fragments and which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, e.g., Ausubel et al., supra). Moreover, many 15 expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence of a polypeptide of the invention (e.g., the signal sequence in any of SEQ ID NOs: 3, 13, 23, 33, 43, 53, 63, 73, and 83) can be used to facilitate 20 secretion and isolation of the secreted protein or another protein of interest. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of 25 the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to the described polypeptides having a signal sequence, as well as to the signal sequence itself and to the polypeptide in the absence of the signal sequence (i.e., the cleavage products). In one embodiment, a

nucleic acid sequence encoding a signal sequence of the invention can be operably linked in an expression vector with a protein of interest, such as a protein which is ordinarily not secreted or is otherwise difficult to isolate. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked with the protein of interest using a sequence which facilitates purification, such as with a GST domain.

In another embodiment, the signal sequences of the present invention can be used to identify regulatory sequences, e.g., promoters, enhancers, repressors. Since signal sequences are the most amino-terminal sequences of a peptide, the nucleic acids which flank the signal sequence on its amino-terminal side are likely regulatory sequences which affect transcription. Thus, a nucleotide sequence which encodes all or a portion of a signal sequence can be used as a probe to identify and isolate signal sequences and their flanking regions, and these flanking regions can be studied to identify regulatory elements therein.

The present invention also pertains to variants of the polypeptides of the invention. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, e.g., discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding with a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring

form of the protein can have fewer side effects in a subject, relative to treatment with the naturally occurring form of the protein.

5 Variants of a protein of the invention which function as either agonists (e.g., mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences can be expressed
10 as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) Tetrahedron 39:3; Itakura et al. (1984) Annu. Rev. Biochem. 53:323; Itakura et al. (1984) Science 198:1056; Ike et al. (1983) Nucleic Acid Res. 11:477).

15 In addition, libraries of fragments of the coding sequence of a polypeptide of the invention can be used to generate a variegated population of polypeptides for screening and subsequent selection of variants. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, re-naturing the DNA to form double stranded DNA which can include sense / antisense
20 pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be

derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan (1992) Proc. Natl. Acad. Sci. USA 89:7811-7815; Delgrave et al. (1993) Protein Engineering 6(3):327-331).

An isolated polypeptide of the invention, or a fragment thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polypeptide or protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 10 (preferably 12, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of any of SEQ ID NOs: 3-8, 13-18, 23-28, 33-38, 43, 53-55, 63-65, 73, and 83-85 or the amino acid sequence encoded by the nucleotide sequence of any of the clones deposited as ATCC® Accession numbers 207185, 207221, PTA-147, PTA-425, PTA-424, ____, and ____, and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein.

Examples of epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, e.g., hydrophilic regions. Figures 1I, 1J, 2F, 3F, 4D, 4G, and 5C are hydrophobicity plots of proteins of the invention. These plots or similar analyses can be used to identify hydrophilic regions.

5 An immunogen typically is used to prepare antibodies by immunizing a suitable (i.e., immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete
10 adjuvant, or a similar immunostimulatory agent.

Accordingly, another aspect of the invention pertains to antibodies directed against a polypeptide of the invention. The terms "antibody" and "antibody substance" as used interchangeably herein refer to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that
15 contain an antigen binding site which specifically binds an antigen, such as a polypeptide of the invention. A molecule which specifically binds with a given polypeptide of the invention is a molecule which binds the polypeptide, but does not substantially bind other molecules in a sample, e.g., a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of
20 immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as papain or pepsin, respectively. The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an
25 antigen binding site capable of immunoreacting with a particular epitope.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques,

Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J.* 12:725-734.

5 Recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described
10 in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al. (1988) *Science* 240:1041-1043; Liu et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al. (1987) *J. Immunol.* 139:3521-
15 3526; Sun et al. (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al. (1987) *Cancer Res.* 47:999-1005; Wood et al. (1985) *Nature* 314:446-449; and Shaw et al. (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi et al. (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones et al. (1986) *Nature* 321:552-525; Verhoeyan et al. (1988) *Science* 239:1534; and Beidler
20 et al. (1988) *J. Immunol.* 141:4053-4060.

 Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The
25 transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during

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B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers et al. (1994) *Bio/technology* 12:899-903).

An antibody directed against a polypeptide of the invention (e.g., monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polypeptide. The antibodies can also be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin / biotin and avidin / biotin;

examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and
5 examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

An antibody (or fragment thereof) can be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent, or a radioactive agent (e.g., a radioactive metal ion). Cytotoxins and cytotoxic agents include any agent that is detrimental to cells. Examples of such agents include taxol, cytochalasin B, gramicidin D,
10 ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g.,
15 methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, and 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin {formerly
20 designated daunomycin} and doxorubicin), antibiotics (e.g., dactinomycin {formerly designated actinomycin}, bleomycin, mithramycin, and anthramycin), and anti-mitotic agents (e.g., vincristine and vinblastine).

Conjugated antibodies of the invention can be used for modifying a given biological response, the drug moiety not being limited to classical chemical
25 therapeutic agents. For example, the drug moiety can be a protein or polypeptide possessing a desired biological activity. Such proteins include, for example, toxins such as abrin, ricin A, Pseudomonas exotoxin, or diphtheria toxin; proteins such as tumor necrosis factor, alpha-interferon, beta-interferon, nerve growth factor, platelet

derived growth factor, tissue plasminogen activator; and biological response modifiers such as lymphokines, interleukin-1, interleukin-2, interleukin-6, granulocyte macrophage colony stimulating factor, granulocyte colony stimulating factor, or other growth factors.

5 Techniques for conjugating a therapeutic moiety to an antibody are well known (see, e.g., Arnon et al., 1985, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al., Eds., Alan R. Liss, Inc. pp. 243-256; Hellstrom et al., 1987, "Antibodies For Drug Delivery", in Controlled Drug Delivery, 2nd ed., Robinson et al., Eds., Marcel Dekker, Inc., pp. 623-653; Thorpe, 1985, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al., Eds., pp. 475-506; "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al., Eds., Academic Press, pp. 303-316, 1985; and Thorpe et al., 1982, Immunol. Rev., 62:119-158). Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

20 III. Recombinant Expression Vectors and Host Cells

 Another aspect of the invention pertains to vectors, including expression vectors, containing a nucleic acid encoding a polypeptide of the invention (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they

are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain
5 vectors, designated expression vectors, are capable of directing expression of genes with which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-
10 associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is
15 operably linked with the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked with the regulatory sequence(s) in a manner which allows expression of the nucleotide sequence (e.g., in an in vitro transcription / translation system or in a host cell when the vector is introduced into the host cell).
20 The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide
25 sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be

transformed, and the level of expression of protein desired. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

5 The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic (e.g., *E. coli*) or eukaryotic cells (e.g., insect cells (using baculovirus expression vectors), yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, supra. Alternatively, the recombinant expression vector can be transcribed and translated in
10 vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

 Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein.
15 Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable
20 separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) Gene 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia,
25 Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

 Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann et al., (1988) Gene 69:301-315) and pET 11d (Studier et al., Gene

Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 60-89). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident lambda prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria having an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector such that the individual codons for each amino acid are those preferentially used in *E. coli* (Wada et al. (1992) Nucleic Acids Res. 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be performed by standard DNA synthesis techniques.

In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari et al. (1987) EMBO J. 6:229-234), pMFa (Kurjan and Herskowitz, (1982) Cell 30:933-943), pJRY88 (Schultz et al. (1987) Gene 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith et al. (1983) Mol. Cell Biol. 3:2156-2165) and the pVL series (Lucklow and Summers (1989) Virology 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian

polypeptide of the invention. Regulatory sequences operably linked with a nucleic acid cloned in the antisense orientation can be selected which direct continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be selected which direct
 5 constitutive, tissue specific, or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of
 10 gene expression using antisense genes see Weintraub et al. (Reviews - Trends in Genetics, Vol. 1(1) 1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is
 15 understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications can occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

20 A host cell can be any prokaryotic (e.g., E. coli) or eukaryotic cell (e.g., insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-
 25 recognized techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, and electroporation. Suitable methods for transforming or

transfecting host cells can be found in Sambrook, et al. (supra), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., for resistance to antibiotics) can be introduced into the host cells along with the gene of interest. Examples of selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene survive, while other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide of the invention using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can be used to produce non-human transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a polypeptide of the invention have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a polypeptide of the invention have been introduced into their genome or homologous recombinant animals in which endogenous encoding a polypeptide of the invention sequences have been altered. Such animals are useful for studying the function and/or activity of the polypeptide and for identifying and/or evaluating modulators of polypeptide

transgene in tissues or cells of the animals. A transgenic founder animal can be used to breed additional animals carrying the transgene. Moreover, transgenic animals harboring the transgene can further be bred to other transgenic animals harboring other transgenes.

5 To create an homologous recombinant animal, a vector is prepared which contains at least a portion of a gene encoding a polypeptide of the invention into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the gene. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (i.e.,
10 no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered, but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the
15 altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases
20 of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi (1987) Cell 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, e.g., Li et al. (1992) Cell
25 69:915). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras (see, e.g., Bradley in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, Robertson, ed. (IRL, Oxford, 1987) pp. 113-152). A chimeric embryo can then be implanted into a suitable

typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, anti-bacterial and anti-fungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a polypeptide or nucleic acid of the invention. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid of the invention. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid of the invention and one or more additional active compounds.

The agent which modulates expression or activity can, for example, be a small molecule. For example, such small molecules include peptides, peptidomimetics, amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 500 grams per

mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the ken of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention.

Examples of doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). Examples of doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or about 1 milligram per kilogram to about 50 milligrams per kilogram). For antibodies, examples of dosages are from about 0.1 milligram per kilogram to 100 milligrams per kilogram of body weight (generally 10 milligrams per kilogram to 20 milligrams per kilogram). If the antibody is to act in the brain, a dosage of 50 milligrams per kilogram to 100 milligrams per kilogram is usually appropriate. It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low

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dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted using acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). The composition should be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and should be preserved against the contaminating action of

microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various anti-bacterial and anti-fungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium, and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, examples of methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the

compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, adjuvant materials, or both, can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate,

by stereotactic injection (see, e.g., Chen et al. (1994) Proc. Natl. Acad. Sci. USA 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where
5 the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

It is recognized that the pharmaceutical compositions and methods described herein can be used independently or in combination with one another. That is,
10 subjects can be administered one or more of the pharmaceutical compositions, e.g., pharmaceutical compositions comprising a nucleic acid molecule or protein of the invention or a modulator thereof, subjected to one or more of the therapeutic methods described herein, or both, in temporally overlapping or non-overlapping regimens. When therapies overlap temporally, the therapies may generally occur in
15 any order and can be simultaneous (e.g., administered simultaneously together in a composite composition or simultaneously but as separate compositions) or interspersed. By way of example, a subject afflicted with a disorder described herein can be simultaneously or sequentially administered both a cytotoxic agent which selectively kills aberrant cells and an antibody (e.g., an antibody of the invention)
20 which can, in one embodiment, be conjugated or linked with a therapeutic agent, a cytotoxic agent, an imaging agent, or the like.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

25 V. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologs, and antibodies described herein can be used in one or more of the following methods: a) screening assays; b) detection assays (e.g., chromosomal mapping, tissue typing, forensic

biology); c) predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and d) methods of treatment (e.g., therapeutic and prophylactic). For example, polypeptides of the invention can to used for all of the purposes identified herein in portions of the disclosure relating to individual types of protein of the invention. The isolated nucleic acid molecules of the invention can be used to express proteins (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect mRNA (e.g., in a biological sample) or a genetic lesion, and to modulate activity of a polypeptide of the invention. In addition, the polypeptides of the invention can be used to screen drugs or compounds which modulate activity or expression of a polypeptide of the invention as well as to treat disorders characterized by insufficient or excessive production of a protein of the invention or production of a form of a protein of the invention which has decreased or aberrant activity compared to the wild type protein. In addition, the antibodies of the invention can be used to detect and isolate a protein of the and modulate activity of a protein of the invention.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

A. Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, i.e., candidate or test compounds or agents (e.g., peptides, peptidomimetics, small molecules or other drugs) which bind with a polypeptide of the invention or have a stimulatory or inhibitory effect on, for example, expression or activity of a polypeptide of the invention.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind with or modulate the activity of the membrane-bound form of a polypeptide of the invention or biologically active portion thereof. The test compounds of the present invention can be obtained using any of the numerous

approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer, or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des.* 12:145).

Examples of methods useful for the synthesis of molecular libraries can be found in the art, for example in: DeWitt et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:6909; Erb et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann et al. (1994). *J. Med. Chem.* 37:2678; Cho et al. (1993) *Science* 261:1303; Carrell et al. (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell et al. (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and Gallop et al. (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds can be presented in solution (e.g., Houghten (1992) *Bio/Techniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), chips (Fodor (1993) *Nature* 364:555-556), bacteria (U.S. Patent No. 5,223,409), spores (Patent numbers 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or phage (Scott and Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6378-6382; and Felici (1991) *J. Mol. Biol.* 222:301-310).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of a polypeptide of the invention, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind with the polypeptide is determined. The cell, for example, can be a yeast cell or a cell of mammalian origin. Determining the ability of the test compound to bind with the polypeptide can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the polypeptide or

the ability of the polypeptide to bind with or interact with a target molecule or to transport molecules across the cytoplasmic membrane.

Determining the ability of a polypeptide of the invention to bind with or interact with a target molecule can be accomplished by one of the methods described above for determining direct binding. As used herein, a "target molecule" is a molecule with which a selected polypeptide (e.g., a polypeptide of the invention binds or interacts with in nature, for example, a molecule on the surface of a cell which expresses the selected protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. A target molecule can be a polypeptide of the invention or some other polypeptide or protein. For example, a target molecule can be a component of a signal transduction pathway which facilitates transduction of an extracellular signal (e.g., a signal generated by binding of a compound to a polypeptide of the invention) through the cell membrane and into the cell or a second intercellular protein which has catalytic activity or a protein which facilitates association of downstream signaling molecules with a polypeptide of the invention. Determining the ability of a polypeptide of the invention to bind with or interact with a target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (e.g., an mRNA, intracellular Ca^{2+} , diacylglycerol, IP3, and the like), detecting catalytic / enzymatic activity of the target on an appropriate substrate, detecting induction of a reporter gene (e.g., a regulatory element that is responsive to a polypeptide of the invention operably linked with a nucleic acid encoding a detectable marker, e.g., luciferase), or detecting a cellular response, for example, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a polypeptide of the invention or biologically active

portion thereof with a test compound and determining the ability of the test compound to bind with the polypeptide or biologically active portion thereof. Binding of the test compound with the polypeptide can be determined either directly or indirectly as described above. In one embodiment, the assay includes contacting the polypeptide of the invention or biologically active portion thereof with a known compound which binds the polypeptide to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the polypeptide, wherein determining the ability of the test compound to interact with the polypeptide comprises determining the ability of the test compound to preferentially bind with the polypeptide or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting a polypeptide of the invention or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the polypeptide or biologically active portion thereof. Determining the ability of the test compound to modulate activity of the polypeptide can be accomplished, for example, by determining the ability of the polypeptide to bind with a target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of the polypeptide can be accomplished by determining the ability of the polypeptide of the invention to further modulate the target molecule. For example, the catalytic activity, the enzymatic activity, or both, of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting a polypeptide of the invention or biologically active portion thereof with a known compound which binds the polypeptide to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test

In another embodiment, modulators of expression of a polypeptide of the invention are identified in a method in which a cell is contacted with a candidate compound and expression of the selected mRNA or protein (i.e., mRNA or protein corresponding to a polypeptide or nucleic acid of the invention) in the cell is
5 determined. The level of expression of the selected mRNA or protein in the presence of the candidate compound is compared with the level of expression of the selected mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of expression of the polypeptide of the invention based on this comparison. For example, if expression of the selected
10 mRNA or protein is greater (i.e., statistically significantly greater) in the presence of the candidate compound than in its absence, then the candidate compound is identified as a stimulator of expression of the selected mRNA or protein. Alternatively, if expression of the selected mRNA or protein is less (i.e., statistically significantly less) in the presence of the candidate compound than in its absence,
15 then the candidate compound is identified as an inhibitor of expression of the selected mRNA or protein. The level of the selected mRNA or protein expression in the cells can be determined by methods described herein.

In yet another aspect of the invention, a polypeptide of the invention can be used as a "bait protein" in a two-hybrid assay or three hybrid assay (see, e.g., U.S.
20 Patent No. 5,283,317; Zervos et al. (1993) Cell 72:223-232; Madura et al. (1993) J. Biol. Chem. 268:12046-12054; Bartel et al. (1993) Bio/Techniques 14:920-924; Iwabuchi et al. (1993) Oncogene 8:1693-1696; and PCT Publication No. WO 94/10300), to identify other proteins which bind with or interact with the polypeptide of the invention and modulate activity of the polypeptide of the invention. Such
25 binding proteins are also likely to be involved in the propagation of signals by the polypeptide of the inventions as, for example, upstream or downstream elements of a signaling pathway involving the polypeptide of the invention.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

B. Detection Assays

5 Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue
10 typing); and (iii) aid in forensic identification of a biological sample. These applications are described in the subsections below.

1. Chromosome Mapping

 Once the sequence (or a portion of the sequence) of a gene has been isolated,
15 this sequence can be used to map the location of the gene on a chromosome. Accordingly, nucleic acid molecules described herein or fragments thereof, can be used to map the location of the corresponding genes on a chromosome. Mapping of sequences to chromosomes is an important first step in correlating these sequences with genes associated with occurrence of disease. For example, the TANGO 273
20 gene exhibits significant homology with a portion of chromosome 7 between chromosomal markers D7S2467 and D7S2552.

 Briefly, genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 nucleotide residues in length) from the sequence of a gene of the invention. Computer analysis of the sequence of a gene of the invention can be used
25 to rapidly select primers that do not span more than one exon in the genomic DNA, which would complicate the amplification process. These primers can be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the gene sequences

will yield an amplified fragment. For a review of this technique, see D'Eustachio et al. ((1983) Science 220:919-924).

PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using one or more nucleic acid sequences of the invention to design oligonucleotide primers, sub-localization can be achieved using panels of fragments prepared from specific chromosomes. Other mapping strategies which can similarly be used to map a gene to its chromosomal location include in situ hybridization (described in Fan et al. (1990) Proc. Natl. Acad. Sci. USA 87:6223-27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization with chromosome specific cDNA libraries.

Fluorescence in situ hybridization (FISH) of a DNA sequence using a metaphase chromosomal spread can be used to provide a precise chromosomal location in one step. For a review of this technique, see Verma et al. (Human Chromosomes: A Manual of Basic Techniques (Pergamon Press, New York, 1988)).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on a chromosome. Alternatively, panels of reagents can be used for marking multiple sites, multiple chromosomes, or both. Reagents corresponding to non-coding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross-hybridization during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, Mendelian Inheritance in Man, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified by linkage analysis (co-inheritance of

physically adjacent genes), described in, e.g., Egeland et al. (1987) Nature 325:783-787.

Moreover, differences in the DNA sequences between individuals affected and non-affected with a disease associated with a gene of the invention can be determined. If a mutation is observed in some or all of the affected individuals, but not in any (or in very few) non-affected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and non-affected individuals generally involves first looking for structural alterations in the chromosomes such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

2. Tissue Typing

The nucleic acid sequences of the present invention can also be used to identify individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. This method does not suffer from the current limitations of physical identification devices such as general issue "dog tags," which can be lost, switched, or stolen, making positive identification difficult. The sequences of the present invention are useful as additional DNA markers for RFLP (described in U.S. Patent 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique which determines the actual base-by-base DNA sequence of selected portions of an individual's genome. The nucleic acid sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the

sequences. These primers can then be used to amplify an individual's DNA and to subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, because (with the exception of identical twins) every individual has a unique set of such DNA sequences owing, at least in part, to allelic differences. Sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The nucleic acid sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the non-coding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per 500 nucleotide residues. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the non-coding regions, fewer non-coding sequences are necessary to differentiate individuals. The non-coding sequences of any of SEQ ID NOs: 1, 11, 21, 31, 41, 51, 61, 71, and 81 can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers which each yield a non-coding amplified sequence of 100 bases. If predicted coding sequences, such as those in any of SEQ ID NOs: 2, 12, 22, 32, 42, 52, 62, 72, and 82 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

If a panel of reagents from the nucleic acid sequences described herein is used to generate a unique identification database for an individual, those same reagents can later be used to identify nucleic acids, cells, or tissue from that individual. Using the unique identification database, positive identification of the individual, living or dead, can be made from extremely small samples.

3. Use of Partial Gene Sequences in Forensic Biology

DNA-based identification techniques can be used in forensic biology.

Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues (e.g., hair or skin) or body fluids (e.g., blood, saliva, or semen) found at a crime scene. The amplified sequence can be compared with a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents (e.g., PCR primers) targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e., another DNA sequence that is unique to a particular individual). As mentioned above, actual nucleotide sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme-generated fragments. Sequences of non-coding regions are particularly appropriate for this use, because greater numbers of polymorphisms occur in non-coding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the nucleic acid sequences of the invention or portions thereof, e.g., fragments derived from non-coding regions having a length of at least 20 or 30 nucleotide residues.

The nucleic acid sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example, an in situ hybridization technique, to identify a specific tissue, e.g., brain tissue. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such probes can be used to identify tissue by species and/or by organ type.

C. Predictive Medicine

5 The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining expression of a gene encoding a polypeptide of the invention as well as activity of a polypeptide of the invention, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant or unwanted expression of a gene encoding a polypeptide of the invention or aberrant or unwanted activity of a polypeptide of the invention. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with a protein of the invention, with expression of a nucleic acid encoding a polypeptide of the invention, or with activity of a polypeptide of the invention. For example, mutations in a gene encoding a polypeptide of the invention can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with a polypeptide of the invention, expression of a nucleic acid encoding it, or its activity.

20 As an alternative to making determinations based on the absolute expression level of selected genes, determinations may be based on the normalized expression levels of these genes. Expression levels are normalized by correcting the absolute expression level of a gene encoding a polypeptide of the invention by comparing its expression to the expression of a different gene, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene. This normalization allows the comparison of the expression

level in one sample (e.g., a patient sample), to another sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a gene, the level of expression of the gene is determined for 10 or more samples of different endothelial (e.g., intestinal endothelium, airway endothelium, or other mucosal epithelium) cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the gene(s) in question. The expression level of the gene determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that gene. This provides a relative expression level and aids in identifying extreme cases of disorders associated with aberrant expression of a gene encoding a polypeptide of the invention protein or with aberrant expression of a ligand thereof.

Preferably, the samples used in the baseline determination will be from either or both of cells which aberrantly express a gene encoding a polypeptide of the invention or a ligand thereof (i.e. 'diseased cells') and cells which express a gene encoding a polypeptide of the invention at a normal level or a ligand thereof (i.e. 'normal' cells). The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether aberrance in expression of a gene encoding a polypeptide of the invention occurs specifically in diseased cells. Such a use is particularly important in identifying whether a gene encoding a polypeptide of the invention can serve as a target gene. In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from endothelial cells (e.g., mucosal endothelial cells) provides a means for grading the severity of the disorder.

Another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, antibodies, antisense oligonucleotides, or other compounds) on the expression or activity of a polypeptide of the invention in clinical trials.

These and other agents are described in further detail in the following sections.

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1. Diagnostic Assays

10 An example of a method for detecting the presence or absence of a polypeptide or nucleic acid of the invention in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting a polypeptide or nucleic acid (e.g., mRNA, genomic DNA) of the invention. An example of an agent for detecting mRNA or genomic DNA encoding a polypeptide of the invention is a labeled nucleic acid probe capable of hybridizing with mRNA or genomic DNA encoding a polypeptide of the invention. The nucleic acid probe can be, for example, a full-length cDNA, such as the nucleic acid of one of SEQ ID NOs: 1, 11, 21, 31, 41, 51, 61, 71, and 81, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions with a mRNA or genomic DNA encoding a polypeptide of the invention. Other suitable probes for use in the diagnostic assays of the invention are described herein.

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An example of an agent for detecting a polypeptide of the invention is an antibody capable of binding with a polypeptide of the invention, such as an antibody having a detectable label. Antibodies can be polyclonal or, preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled," with regard to the probe or antibody, includes direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by coupling it with another reagent that is directly labeled. Examples of indirect labeling include

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detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells, and biological fluids isolated from a subject, as well as tissues, cells, and fluids present within a subject. That is, the detection method of the invention can be used to detect mRNA, protein, or genomic DNA in a biological sample in vitro as well as in vivo. For example, in vitro techniques for detection of mRNA include Northern hybridization methods and in situ hybridization methods. In vitro techniques for detection of a polypeptide of the invention include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitation, and immunofluorescence. In vitro techniques for detection of genomic DNA include Southern hybridizations. Furthermore, in vivo techniques for detection of a polypeptide of the invention include introducing into a subject a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker, the presence and location of which in a subject can be detected using standard imaging techniques.

In one embodiment, the biological sample contains protein molecules obtained from the test subject. Alternatively, the biological sample can contain mRNA molecules obtained from the test subject or genomic DNA molecules obtained from the test subject. An example of a biological sample is a peripheral blood leukocyte-containing sample obtained by conventional means from a subject (e.g., isolated peripheral blood leukocytes).

In another embodiment, the methods further involve obtaining a control biological sample from a control (i.e., non-afflicted) subject, contacting the control sample with a compound or agent capable of detecting a polypeptide of the invention or mRNA or genomic DNA encoding a polypeptide of the invention. The presence or amount of the polypeptide, mRNA, or genomic DNA encoding the polypeptide in

the control and test samples can be compared to assess the degree, if any, to which the presence or amount in the test sample differs from that in the control sample.

The invention also encompasses kits for detecting the presence of a polypeptide or nucleic acid of the invention in a biological sample obtained from a subject. Such kits can be used to determine if a subject is suffering from or is at increased risk of developing a disorder associated with aberrant expression of a polypeptide of the invention (e.g., one of the disorders described in the section of this disclosure wherein the individual polypeptide of the invention is discussed). For example, the kit can comprise a labeled compound or agent capable of detecting the polypeptide or mRNA encoding the polypeptide in a biological sample. The kit can also, or alternatively, contain means for determining the amount of the polypeptide or mRNA in the sample (e.g., an antibody which specifically binds with the polypeptide or an oligonucleotide probe which binds with a nucleic acid encoding the polypeptide). Kits can include instructions for assessing whether the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of the polypeptide if the amount of the polypeptide or mRNA encoding the polypeptide is above or below a normal level.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) which specifically binds with a polypeptide of the invention; and, optionally, (2) a second, different antibody which specifically binds with either the polypeptide or the first antibody and is conjugated with a detectable agent.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide (e.g., a detectably labeled oligonucleotide) which hybridizes with a nucleic acid encoding a polypeptide of the invention or (2) a pair of primers useful for amplifying a nucleic acid encoding a polypeptide of the invention. The kit can comprise, for example, a buffering agent, a preservative, or a protein stabilizing agent. The kit can also comprise components necessary for detecting the detectable

agent (e.g., an enzyme or a substrate). The kit can contain a control sample or a series of control samples which can be assayed and compared with the test sample assay results. Each component of the kit can be enclosed within an individual container and all of the various containers can furthermore be within a single package, optionally with instructions for assessing whether the tested subject is suffering from or is at risk of developing a disorder associated with aberrant expression of the polypeptide.

2. Prognostic Assays

The methods described herein can furthermore be used as diagnostic or prognostic assays to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of a polypeptide of the invention (e.g., one of the disorders described in the section of this disclosure wherein the individual polypeptide of the invention is discussed). Thus, the present invention provides a method in which a test sample is obtained from a subject and a polypeptide or nucleic acid (e.g., mRNA, genomic DNA) of the invention is detected, wherein the presence, level, or activity of the polypeptide or nucleic acid in the sample is associated with an enhanced or diminished risk of developing a disease or disorder associated with aberrant expression or activity of the polypeptide.

Furthermore, the prognostic assays described herein can be used to determine whether an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) can be administered to a subject in order to treat a disease or disorder associated with aberrant expression or activity of a polypeptide of the invention. For example, such methods can be used to determine whether a subject can be effectively treated using a specific agent or class of agents (e.g., agents of a type which decrease activity of the polypeptide). Thus, the present invention provides methods for determining whether an agent can be administered to a subject in order to effectively treat a disorder associated with

aberrant expression or activity of a polypeptide of the invention. When efficacious agents are known or found, such assays can also be used to estimate an efficacious dose of the agent.

The methods of the invention can be used to detect genetic lesions or mutations in a gene of the invention in order to assess if a subject having the lesioned or mutated gene is at risk for a disorder characterized by aberrant expression or activity of a polypeptide of the invention. In certain embodiments, the methods include detecting, in a sample of cells obtained from the subject, the presence or absence of a genetic lesion or mutation characterized by at least one of an alteration affecting the integrity of a gene encoding the polypeptide of the invention, or the mis-expression of the gene encoding the polypeptide of the invention. For example, such genetic lesions or mutations can be detected by ascertaining the existence of at least one of: 1) a deletion of one or more nucleotides from the gene; 2) an addition of one or more nucleotides to the gene; 3) a substitution of one or more nucleotides of the gene; 4) a chromosomal rearrangement of the gene; 5) an alteration in the level of a messenger RNA transcript of the gene; 6) an aberrant modification of the gene, such as of the methylation pattern of the genomic DNA; 7) a non-wild type splicing pattern of a messenger RNA transcript of the gene; 8) a non-wild type level of the protein encoded by the gene; 9) an allelic loss of the gene; and 10) an inappropriate post-translational modification of the protein encoded by the gene. As described herein, there are a large number of assay techniques known in the art which can be used for detecting such lesions and mutations in a gene.

In certain embodiments, detection of the lesion involves the use of an oligonucleotide primer in a polymerase chain reaction (PCR; see, e.g., U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR; see, e.g., Landegran et al. (1988) Science 241:1077-1080; and Nakazawa et al. (1994) Proc. Natl. Acad. Sci. USA 91:360-364), the latter of which can be particularly useful for detecting point mutations in a

gene (see, e.g., Abravaya et al. (1995) *Nucleic Acids Res.* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA, or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize with the selected gene under conditions such that hybridization and amplification of the gene (if present) occurs, and detecting the presence or absence of an amplification product. The method can also include detecting the size of the amplification product and comparing the length to the length of a corresponding product obtained in the same manner from a control sample. PCR, LCR, or both can be used as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self-sustained sequence replication (Guatelli et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi et al. (1988) *Bio/Technology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using any of a variety of techniques well known to those of skill in the art. These detection schemes are especially useful for detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a selected gene can be identified in a sample by detecting alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, (optionally) amplified, digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates occurrence of mutations or other sequence differences in the sample DNA. Moreover, sequence specific ribozymes (see, e.g., U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations are identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, with high density arrays containing hundreds or thousands of oligonucleotide probes (Cronin et al. (1996) Human Mutation 7:244-255; Kozal et al. (1996) Nature Medicine 2:753-759). For example, genetic mutations can be identified using two-dimensional arrays of light-generated DNA probes fixed to a surface, as described in Cronin et al., supra. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by hybridization of the nucleic acid sample with a second hybridization array in order to characterize specific mutations using smaller, specialized probe arrays complementary to many or all potential variants or mutations. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing methods known in the art can be used to directly sequence the selected gene and detect mutations by comparing the sequence of the sample nucleic acids with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert ((1977) Proc. Natl. Acad. Sci. USA 74:560) or Sanger ((1977) Proc. Natl. Acad. Sci. USA 74:5463). It is also contemplated that any of a variety of automated sequencing procedures can be used when performing the diagnostic assays ((1995) Bio/Techniques 19:448), including sequencing by mass spectrometry (see, e.g., PCT Publication No. WO 94/16101; Cohen et al. (1996) Adv. Chromatogr. 36:127-162; and Griffin et al. (1993) Appl. Biochem. Biotechnol. 38:147-159).

Other methods for detecting mutations in a selected gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA /

RNA or RNA / DNA heteroduplexes (Myers et al. (1985) Science 230:1242). In general, the technique of mismatch cleavage entails providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing the wild-type sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as those which exist due to base pair mismatches between the control and sample strands. RNA / DNA duplexes can be treated with RNase to digest mismatched regions, and DNA / DNA hybrids can be treated with S1 nuclease to digest mismatched regions.

In other embodiments, DNA / DNA or RNA / DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is separated by size on denaturing polyacrylamide gels to determine the site of the mutated or mismatched region. See, e.g., Cotton et al. (1988) Proc. Natl. Acad. Sci. USA 85:4397; Saleeba et al. (1992) Methods Enzymol. 217:286-295. In one embodiment, the control DNA or RNA is labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called DNA mismatch repair enzymes) in defined systems for detecting and mapping point mutations in cDNAs obtained from samples of cells. For example, the mutY enzyme of E. coli cleaves following A residues at G / A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves following T residues at G / T mismatches (Hsu et al. (1994) Carcinogenesis 15:1657-1662). According to one embodiment, a probe based on a selected sequence, e.g., a wild-type sequence, is hybridized with a cDNA or other DNA product obtained from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, are detected using an electrophoresis protocol or another polynucleotide-separating method. See, e.g., U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility are used to identify mutations in genes. For example, single strand conformation polymorphism (SSCP) analysis can be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al. (1989) Proc. Natl. Acad. Sci. USA 86:2766; see also Cotton (1993) Mutat. Res. 285:125-144; Hayashi (1992) Genet. Anal. Tech. Appl. 9:73-79). Single-stranded DNA fragments of sample and control nucleic acids are denatured and allowed to re-nature. The secondary structure of single-stranded nucleic acids varies according to their nucleotide sequence, and the resulting alteration in electrophoretic mobility enables detection of even a single base change. The DNA fragments can be labeled or detected using labeled probes. The sensitivity of the assay can be enhanced by using RNA (rather than DNA), because the secondary structure of RNA is more sensitive to sequence changes. In one embodiment, the method uses heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al. (1991) Trends Genet. 7:5).

In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE), as described (Myers et al. (1985) Nature 313:495). When DGGE is used as the method of analysis, DNA is modified to ensure that it does not completely denature, for example by adding a 'GC clamp' of approximately 40 nucleotide residues of high-melting GC-rich DNA to one or both ends of the DNA strands, for example using a PCR method. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) Biophys. Chem. 265:12753).

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, and selective primer extension. For example, oligonucleotide primers can be prepared in

which the known mutation is located centrally. The primers are hybridized with target DNA under conditions which permit hybridization only if a perfect complementary nucleotide sequence match occurs (Saiki et al. (1986) Nature 324:163); Saiki et al. (1989) Proc. Natl. Acad. Sci. USA 86:6230). Such allele
5 specific oligonucleotides are hybridized with PCR-amplified target DNA or attached to a surface for hybridization.

Alternatively, allele specific amplification technology can be used in conjunction with the methods of the invention. Oligonucleotides used as primers for specific amplification have a sequence complementary to the nucleotide sequence of
10 a mutation of interest in the center of the molecule, so that occurrence of amplification depends on occurrence of the mutation in the sample nucleic acid (Gibbs et al. (1989) Nucleic Acids Res. 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatching can prevent or inhibit polymerase extension (Prossner (1993) Tibtech 11:238). In addition, it can be
15 desirable to introduce a novel restriction site in the region of the mutation in order to facilitate cleavage-based detection (Gasparini et al. (1992) Mol. Cell Probes 6:1). Amplification can be performed using Taq ligase (Barany (1991) Proc. Natl. Acad. Sci. USA 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, thereby making it possible to assess the presence of a
20 known mutation at a specific site by looking for the presence or absence of amplification.

The methods described herein can be performed, for example, using pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein. Such kits can be used, for example, in clinical settings to
25 diagnose patients exhibiting symptoms or a family history of a disorder involving a gene encoding a polypeptide of the invention. Furthermore, any cell type or tissue in which the polypeptide of the invention is expressed (e.g., a blood sample containing

peripheral blood leukocytes for proteins which are secreted or which occur on or in peripheral blood leukocytes) can be used in the prognostic assays described herein.

3. Pharmacogenomics

5 Agents which have a stimulatory or inhibitory effect on activity or expression of a polypeptide of the invention, as identified by a screening assay described herein for example, can be administered to individuals to treat (prophylactically or therapeutically) disorders associated with aberrant activity of the polypeptide. In conjunction with such treatment, the pharmacogenomics (i.e., the study of the
10 relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual can be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits selection of
15 effective agents (e.g., drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of a polypeptide of the invention, expression of a nucleic acid of the invention, or mutation content of a gene of the invention in an individual can be
20 determined to facilitate selection of one or more appropriate agents for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Linder (1997) Clin. Chem. 43(2):254-266. In general, two types
25 of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism." These

pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 {NAT 2} and cytochrome P450 enzymes CYP2D6 and CYP2C19) explains why some patients do not obtain the expected drug effects or exhibit exaggerated drug response and serious toxicity following administration of standard and safe doses of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene encoding CYP2D6 is highly polymorphic, and several mutations have been identified in PM. Each of these mutations results in absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, activity of a polypeptide of the invention, expression of a nucleic acid encoding the polypeptide, or mutation content of a gene encoding the polypeptide in an individual can be determined to facilitate selection of appropriate agents for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-

metabolizing enzymes to identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of activity or expression of the polypeptide, such as a modulator identified by one of the screening assays described herein.

4. Monitoring of Effects During Clinical Trials

Monitoring the influence of agents (e.g., drug compounds) on expression or activity of a polypeptide of the invention (e.g., ability to modulate aberrant cell proliferation chemotaxis, differentiation, or both) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent, as determined by a screening assay as described herein, to increase gene expression, protein levels, or protein activity can be monitored in clinical trials of subjects exhibiting decreased gene expression, protein levels, or protein activity.

Alternatively, the effectiveness of an agent, as determined by a screening assay, to decrease gene expression, protein levels, or protein activity can be monitored in clinical trials of subjects exhibiting increased gene expression, protein levels, or protein activity. In such clinical trials, expression or activity of a polypeptide of the invention and, optionally, that of other polypeptide that have been implicated in similar disorders, can be used as a marker of the immune responsiveness of a particular cell.

For example, genes (including those of the invention) that are modulated in cells by treatment with an agent (e.g., a peptide, a drug, or another small molecule) which modulates activity or expression of a polypeptide of the invention (e.g., as identified in a screening assay described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and their RNA can be prepared and analyzed to determine the

level of expression of one or more genes of the invention and, optionally, other genes implicated in the disorder. The levels of gene expression (i.e., a gene expression pattern) can be quantified by Northern blot analysis or by RT-PCR, as described herein, or by assessing the amount of protein produced, by one of the methods as described herein, or by measuring the level of activity of a gene of the invention or other gene(s). In this way, the gene expression pattern can serve as an indicator of the physiological response of the cells to the agent. Accordingly, this response state can be determined before, and at various points during, or after treatment of the individual with the agent (or, of course, at more than one of these stages).

In one embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of the polypeptide or nucleic acid of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level the of the polypeptide or nucleic acid of the invention in the post-administration sample(s); (v) comparing the level of the polypeptide or nucleic acid of the invention in the pre-administration sample with the level of the polypeptide or nucleic acid of the invention in the post-administration sample(s); and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent can be desirable to increase the expression or activity of the polypeptide to levels higher than those detected, i.e., to increase the effectiveness of the agent. Alternatively, decreased administration of the agent can be desirable to decrease expression or activity of the polypeptide to levels lower than those detected, i.e., to decrease the effectiveness of the agent.

C. Methods of Treatment

The present invention provides both prophylactic and therapeutic methods of treating a subject afflicted with, at risk for developing, or susceptible to a disorder associated with aberrant expression or activity of a polypeptide of the invention.

5 Such disorders are described elsewhere in this disclosure.

1. Prophylactic Methods

In one aspect, the invention provides a method for preventing in a subject, a disorder associated with aberrant expression or activity of a polypeptide of the invention, by administering to the subject an agent which modulates expression of the polypeptide or at least one activity of the polypeptide. Subjects at risk for a disease which is caused or contributed to by aberrant expression or activity of a polypeptide of the invention can be identified by, for example, any one or combination of the diagnostic and prognostic assays described herein.

10 Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the aberrance, so that the disease or disorder is prevented or, alternatively, delayed in its onset or progression. Depending on the type of aberrance, for example, an agonist or antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays

15 described herein.

20

2. Therapeutic Methods

Another aspect of the invention pertains to methods of modulating expression or activity of a polypeptide of the invention for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of the polypeptide. An agent that modulates activity can be an agent as described herein, such as a nucleic acid, or a protein, a naturally-occurring cognate ligand of the polypeptide, a peptide, a peptidomimetic,

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or a small molecule. In one embodiment, the agent stimulates one or more of the biological activities of the polypeptide. Examples of such stimulatory agents include a polypeptide of the invention, a biologically active portion of such a polypeptide, a portion of such a polypeptide which comprises an epitope of the native polypeptide, and a nucleic acid molecule encoding the polypeptide of the invention that has been introduced into the cell. In another embodiment, the agent inhibits a biological activity of the polypeptide of the invention or expression of a protein or nucleic acid of the invention. Examples of such inhibitory agents include antisense nucleic acid molecules and antibodies. These modulatory methods can be performed in vitro (e.g., by culturing the cell with the agent) or, alternatively, in vivo (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a polypeptide of the invention. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., up-regulates or down-regulates) expression or activity. In another embodiment, the method involves administering a polypeptide of the invention or a nucleic acid molecule of the invention as therapy to compensate or substitute for reduced or aberrant expression or activity of the polypeptide.

Stimulation of activity is desirable in situations in which activity or expression is abnormally low or in which increased activity is likely to have a beneficial effect. Conversely, inhibition of activity is desirable in situations in which activity or expression is abnormally high or in which decreased activity is likely to have a beneficial effect.

The contents of all references, patents, and published patent applications cited in this disclosure are hereby incorporated by reference.

Deposits of Clones

Clone containing one or more cDNA molecules encoding polypeptides of the invention have been deposited with the American Type Culture Collection (ATCC®; 10801 University Boulevard, Manassas, VA 20110-2209) on dates disclosed herein, and these deposits were assigned the Accession Numbers disclosed herein. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. These deposits were made merely as a convenience for those of skill in the art and are not an admission that any deposit is required in order to comply with 35 U.S.C. §112.

Where a clone containing multiple cDNA molecules was deposited, the following standard digest procedure can be used to liberate fragments corresponding to individual cDNA molecules, except as otherwise described. To isolate the cDNA clone, an aliquot of the deposited clone can be streaked out to yield single colonies on nutrient medium (e.g., Luria broth plates) supplemented with 100 micrograms per milliliter ampicillin. Single colonies are grown, and plasmid DNA is extracted from single colonies using a standard mini-preparation procedure. Next, a sample of the DNA mini-preparation is digested using a combination of the restriction enzymes Sal I and Not I, and the resulting products are resolved on a 0.8% (w/v) agarose gel using standard DNA electrophoresis conditions.

Clone EpT273, encoding human TANGO 273 was deposited with ATCC® on April 2, 1999 and was assigned Accession Number 207185.

Clones containing cDNA molecules encoding murine TANGO 273 were deposited with ATCC® on April 21, 1999 and were assigned Accession Number 207221, as part of a composite deposit representing a mixture of five strains, each carrying one recombinant plasmid harboring a particular cDNA clone. The standard digest procedure (except that restriction enzymes SalI, NotI, and ApaI are used) liberates a fragment as follows:

mouse TANGO 273 (clone EpTm273): .3 kilobase and 2.6 kilobase
(mouse TANGO 273 has a Apa I cut site at about base pair 298).

The identity of the strain can be inferred from the fragment liberated.

Clones comprising cDNA molecules encoding human TANGO 325 were
5 deposited with ATCC® on May 28, 1999, as part of a composite deposit representing a
mixture of five strains, each carrying one recombinant plasmid harboring a particular
cDNA clone. This deposit was assigned Accession Number PTA-147. The standard
digest procedure (except that restriction enzymes Sall, NotI, and SmaI are used)
liberates a fragment as follows:

10 human TANGO 325 (clone EpT325): 2.2 kilobases

The identity of the strain can be inferred from the fragment liberated.

Clones containing cDNA molecules encoding TANGO 364 (clones Aped),
were deposited with ATCC® on July 23, 1999 as Accession No. PTA-425, as part of a
composite deposit representing a mixture of three strains, each carrying one
15 recombinant plasmid harboring a particular cDNA clone. The standard digest
procedure liberates a fragment as follows:

TANGO 364 (Aped): 3.5 kilobase pairs

The identity of the strain can be inferred from the fragment liberated.

Clones containing cDNA molecules encoding TANGO 405 (including clone
20 405), were deposited with ATCC® on July 23, 1999 as Accession No. PTA-424, as
part of a composite deposit representing a mixture of five strains, each carrying one
recombinant plasmid harboring a particular cDNA clone. The standard digest
procedure liberates a fragment as follows:

TANGO 405 (405): 3.1 kilobase pairs

25 The identity of the strain can be inferred from the fragment liberated.

A clone encoding murine TANGO 405 was deposited with ATCC® on ____ and
was assigned Accession Number ____.

A clone encoding human M019 was deposited with ATCC® on ____ and was assigned Accession Number ____.

Equivalents

- 5 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the embodiments of the invention described herein. Such equivalents are encompassed by the following claims.

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